STIC-Bi t ch/Ch mLib 76052

From: O'Hara, Eileen
Sent: Wednesday, September 18, 2002 5:39 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request for 09/746,375

SEARCH REQUEST FORM-SEQUENCE

Examiner: Eileen O'Hara (Room 10E18) Art Unit 1646

Serial Number: **09/746,375**
Novel Cytokine ZCYTO18
Presnell et al

Date: 09/18/02 Phone: 308-3312 CM1 10A01 **mailbox 10C01**

Please search the following:

SEQ ID NO: 1

also, 14 contiguous nucleotides of SEQ ID NO: 1

in **commercial and interference** databases.

Please put results on paper.

Thank you!

Eileen

Eileen B. O'Hara
CM1 10A01 mailbox 10C01
703-308-3312
U.S. Patent and Trademark Office
Art Unit 1646
eileen.o'hara@uspto.gov

RECEIVED
SEP 19 2002
STIC

10019

Edward Hart
Technicai Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 9/19/02
Date Completed: 9/23/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 2
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 04
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:43:59 ; Search time 217.46 Seconds
(without alignments)
8811.168 Million cell updates/sec

Title: US-09-746-375-1
Perfect score: 1116
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttggatatccta 1116

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 14

Total number of hits satisfying chosen parameters: 19226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_032802:*
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23: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1116	100.0	1116	22	AAD09719	Human cytokine, ZC
2	1116	100.0	1116	22	AAF83741	Human IL-TIF polyp
3	1116	100.0	1177	21	AAC81773	Human GIL-19/AE289
4	1114	99.8	1152	22	AAF92134	Human PRO10096 cDN
5	1114	99.8	1152	22	AAC87053	Nucleotide sequenc
6	1090	97.7	1132	22	AAC84310	Human EXCS encodin
7	934	83.7	1139	22	AAF28841	Human interleukin-
8	639	57.3	690	21	AAA28839	Human T cell induc
9	639	57.3	690	22	AAS14875	Human cDNA encodin
10	207	18.5	4796	21	AAA28840	Human T cell induc
11	207	18.5	4797	22	AAS14876	Human partial geno
12	35	3.1	778	22	AAD09746	Mouse ZCYTO18 cDNA
13	35	3.1	1119	21	AAA28815	Murine T cell indu
14	35	3.1	1119	22	AAS14858	Mouse cDNA encodin
15	35	3.1	1166	21	AAC81774	Murine GIL-19 prot
16	31	2.8	7444	21	AAA28816	Murine T cell indu
17	31	2.8	7445	22	AAS14859	Mouse partial geno
18	28	2.5	1111	21	AAA28817	Murine T cell indu
19	28	2.5	1111	22	AAS14860	Mouse cDNA for T c
20	28	2.5	5935	21	AAA28818	Murine T cell indu
21	28	2.5	5935	22	AAS14878	Mouse partial geno
22	27	2.4	36	22	AAD09730	Human ZCYTO18 cDNA
23	27	2.4	36	22	AAF83753	Human IL-TIF cDNA
c 24	24	2.2	24	22	AAD09721	PCR primer, ZC2584
25	24	2.2	24	22	AAD09722	PCR primer, ZC2584
c 26	24	2.2	33	22	AAD09731	Human ZCYTO18 cDNA
c 27	24	2.2	33	22	AAF83754	Human IL-TIF cDNA
28	24	2.2	5421	24	ABL32132	Human immune syste
c 29	23	2.1	23	22	AAD09724	ZC25839 PCR primer
c 30	23	2.1	37	22	AAD09734	Human ZCYTO18 cDNA
c 31	22	2.0	22	21	AAA28831	Primer for human T
c 32	22	2.0	22	22	AAS14867	Human T cell deriv
33	22	2.0	39	22	AAD09733	Human ZCYTO18 cDNA
c 34	22	2.0	2640	22	AAH76178	A. thaliana SGT101
c 35	22	2.0	2671	22	AAH76176	A. thaliana SGT101
c 36	21	1.9	21	21	AAA28833	5' RACE primer for
c 37	21	1.9	21	21	AAA28834	5' RACE primer for
c 38	21	1.9	21	22	AAS14869	Human T cell deriv
c 39	21	1.9	21	22	AAS14870	Human T cell deriv
c 40	21	1.9	706	22	AAH57394	Human skeletal mus
41	21	1.9	3126	21	AAA70143	Plasmodium falcipa
42	21	1.9	15768	24	ABL33171	Human immune syste
43	21	1.9	16217	24	ABL32625	Human immune syste
44	20	1.8	473	22	ABA43453	Human breast cell
45	20	1.8	473	22	ABA53906	Human foetal liver

ALIGNMENTS

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ID   AAD09719 standard; cDNA; 1116 BP.
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AC   AAD09719;
XX
DT   10-SEP-2001  (first entry)
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DE   Human cytokine, ZCYTO18 cDNA.
XX
KW   Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW   cancer; inflammation; gene therapy; chromosome 12; ss.
XX
OS   Homo sapiens.
XX
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FT   mat_peptide     120..557
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FT                   /product= "Human mature ZCYTO18 protein #2"
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XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35308.
XX
PR 23-DEC-1999; 99US-0471767.
PR 01-DEC-2000; 2000US-0250841.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
DR P-PSDB; AAE04538, AAE04539.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer
XX
PS Claim 2; Page 140-142; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC killing cancer cells. It is useful for increasing platelets in a
CC patient or injured tissue. It is also used in gene therapy.
CC The present sequence is a cDNA encoding novel human cytokine, ZCYTO18
CC protein. ZCYTO18 DNA is located at the 12q15 region of chromosome 12.
XX
SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 100.0%; Score 1116; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
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AC AAF83741;
XX
DT 23-JUL-2001 (first entry)
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DE Human IL-TIF polypeptide encoding cDNA.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 21..560
FT /*tag= a
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XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32703.
XX
PR 03-DEC-1999; 99US-0169049.
PR 13-SEP-2000; 2000US-0232219.
PR 31-OCT-2000; 2000US-0244610.

XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
DR P-PSDB; AAB62664.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions -
XX
PS Example 17; Page 193-195; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents a cDNA encoding
CC the human IL-TIF protein.
XX
SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 100.0%; Score 1116; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
AAC81773
ID AAC81773 standard; cDNA; 1177 BP.
XX
AC AAC81773;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human GIL-19/AE289 protein coding sequence.
XX
KW Human; GIL-19/AE289; IL-10; interleukin-10; nutrition;
KW cell proliferation; immune stimulation; immune suppression;
KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200065027-A2.
XX
PD 02-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11479.
XX
PR 28-APR-1999; 99US-0131473.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Fouser L, Spaulding V, Xuan D;
XX
DR WPI; 2000-687325/67.
DR P-PSDB; AAB36292.

```
XX
PT   Human GIL-19 protein that shows a high degree of homology to IL
PT   (interleukin)-10, useful in upregulation of humoral immune responses,
PT   as an antiinflammatory agent and as a modulator of immune responses
PT   associated with injury -
XX
PS   Claim 1; Page 59; 60pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   novel human GIL-19/AE289 protein. The protein shows homology to
CC   interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used
CC   in the regulation of cell proliferation and differentiation,
CC   haematopoiesis, immune stimulation or suppression, tissue growth and
CC   tumour inhibition. In addition, it also has uses in the treatment of
CC   inflammation and in nutrition.
XX
SQ   Sequence 1177 BP; 362 A; 245 C; 232 G; 338 T; 0 other;

  Query Match           100.0%;  Score 1116;  DB 21;  Length 1177;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1116;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      45 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 104

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     105 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 164

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 224

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     225 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 284

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     285 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 344

Qy     301 aggtgctgaacttcaccctgaagaagtgctgttccctcaatctgataggttccagcctt 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     345 aggtgctgaacttcaccctgaagaagtgctgttccctcaatctgataggttccagcctt 404

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     405 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 464

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     465 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 524

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     525 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 584

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     585 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 644

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     645 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 704

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     705 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 764

Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     765 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 824

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaataa 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     825 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaataa 884

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     885 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 944

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     945 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 1004

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1005 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1064

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1065 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1124

Qy    1081 tgtttatttgacctcaataaacacttggatatccta 1116
           ||||||||||||||||||||||||||||||||||||
Db    1125 tgtttatttgacctcaataaacacttggatatccta 1160


RESULT   4
AAF92134
ID   AAF92134 standard; cDNA; 1152 BP.
XX
AC   AAF92134;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO10096 cDNA.
XX
KW   Human; PRO protein; mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   P-PSDB; AAB87602.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping.
XX
```

```
PS   Claim 2; Fig 153; 278pp; English.
XX
CC   The present sequence is the coding sequence for a human PRO polypeptide
CC   (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC   antagonists or anti-PRO antibodies are useful for preparation of a
CC   medicament useful in the treatment of a condition which is responsive to
CC   the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC   protein may also be employed as molecular weight markers for protein
CC   electrophoresis. The PRO coding sequence has applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping.
XX
SQ   Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;


  Query Match             99.8%;  Score 1114;  DB 22;  Length 1152;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 97

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 157

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 217

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 277

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 337

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 397

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 457

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 517

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 577

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 637

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     638 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 697

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     698 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 757

Qy     721 aaccaatgccactttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     758 aaccaatgccactttttgtttataagaccagaaggtagactttctaagcatagatatttat 817

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     818 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 877

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     878 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 937

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     938 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 997

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     998 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1057

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1058 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1117

Qy    1081 tgtttatttgacctcaataaacacttggatatcc 1114
          ||||||||||||||||||||||||||||||||
Db    1118 tgtttatttgacctcaataaacacttggatatcc 1151


RESULT   5
AAC87053
ID   AAC87053 standard; cDNA; 1152 BP.
XX
AC   AAC87053;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human polypeptide PRO10096.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             58..597
FT                   /*tag=  a
FT   sig_peptide     58..156
FT                   /*tag=  b
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
```

PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein DA, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Kljavin IJ, Mather JP, Napier MA, Pan J;
PI Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM;
PI Wood WI, Zhang Z;
XX
DR WPI; 2001-050091/06.
DR P-PSDB; AAB31210.
XX
PT Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT transmembrane polypeptide is useful for gene therapy and identification
PT of related polypeptides
XX
PS Claim 2; Fig 63; 244pp; English.
XX
CC The present sequence encodes a human secreted and transmembrane
CC polypeptide. The specification describes human polypeptides, designated
CC PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC can be modulated with agents that bind to these polypeptides, resulting
CC in the death of the cells. The polynucleotides encoding these
CC polypeptides are useful in the recombinant production of the
CC polypeptides, as a hybridisation probe to screen libraries to isolate
CC homologous sequences, or to map the gene. They may also be used for
CC analysing genetic disorders, and to produce transgenic animals which are
CC useful for the development and screening of therapeutically useful
CC reagents. The polynucleotides can also be used in gene therapy e.g. to
CC replace a defective gene.
XX
SQ Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;

Query Match 99.8%; Score 1114; DB 22; Length 1152;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     38 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 97

Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 157

Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    158 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 217

Qy    181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    218 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 277

Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    278 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 337

Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    338 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 397

Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    398 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 457

Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 517

Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    518 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 577

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    578 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 637

Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    638 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 697

Qy    661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    698 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 757

Qy    721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 817

Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 877

Qy    841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 937

Qy    901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaaga 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaaga 997

Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1057

Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1058 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1117

Qy   1081 tgtttatttgacctcaataaacacttggatatcc 1114
          |||||||||||||||||||||||||||||||||
Db   1118 tgtttatttgacctcaataaacacttggatatcc 1151
```

RESULT 6
AAC84310
ID AAC84310 standard; cDNA; 1132 BP.
XX
AC AAC84310;
XX
DT 19-MAR-2001 (first entry)
XX
DE Human EXCS encoding cDNA (clone ID 5571181CB1).
XX
KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;
KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;
KW antiinfertility; cerebroprotective; nootropic; antiulcer; antifungal;
KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
KW keratolytic; protozoacide; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO200070049-A2.
XX
PD 23-NOV-2000.
XX

PF 19-MAY-2000; 2000WO-US13975.
XX
PR 19-MAY-1999; 99US-0134949.
PR 15-JUL-1999; 99US-0144270.
PR 30-JUL-1999; 99US-0146700.
PR 04-OCT-1999; 99US-0157508.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
PI Azimzai Y, Lu DAM, Patterson C;
XX
DR WPI; 2001-025021/03.
DR P-PSDB; AAB48074.
XX
PT New human extracellular signaling nucleic acids and polypeptides useful
PT for diagnosing, treating and preventing infections and
PT gastrointestinal, neurological, reproductive, and
PT autoimmune/inflammatory disorders -
XX
PS Claim 4; Page 108; 114pp; English.
XX
CC The invention provides human extracellular signaling molecules (EXCS)
CC and polynucleotides which identify and encode EXCS. EXCS can be
CC expressed by standard recombinant methodology. The amino acid and nucleic
CC acid sequences of EXCS are useful for diagnosing, treating and
CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,
CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular
CC disease, stroke), reproductive (infertility, ovulatory defects,
CC endometriosis), autoimmune /inflammatory (actinic keratosis, acquired
CC immunodeficiency syndrome (AIDS), Addison's disease), and cell
CC proliferative disorders including cancers (of the breast, adrenal gland,
CC bone). They may also be used to treat fatal familial insomnia,
CC nutritional and metabolic diseases of the nervous system, myopathies,
CC mental disorders (anxiety, schizophrenia, mood), as well as infections
CC caused by parasites (malaria, leishmania, trypanosoma), viral
CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
CC staphylococcus, bacillus), and fungal (aspergillus, blastomyces,
CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
CC agonists, pharmaceutical compositions, and antibodies may also be used
CC for treating or preventing disorders associated with increased or
CC decreased expression or activity of EXCS. EXCS polynucleotides may also
CC be used to detect and quantify gene expression in biopsied tissues in
CC which expression of EXCS may be correlated with the disease, to determine
CC presence or excess expression of EXCS, to monitor regulation of EXCS
CC levels during therapeutic intervention, to detect the presence of
CC associated disorders, as targets in microarray, to generate hybridization
CC probes, and to detect differences in gene sequences among normal, carrier
CC or affected individuals. Antibodies may also be used in diagnosing
CC disorders, in monitoring patients being treated with EXCS agonists,
CC antagonists or inhibitors. Sequences AAC84293-C84318 represent nucleic
CC acid molecules encoding the EXCS of the invention.
XX
SQ Sequence 1132 BP; 333 A; 240 C; 226 G; 333 T; 0 other;

Query Match 97.7%; Score 1090; DB 22; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      31 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 90

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      91 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 150

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     151 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 210

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 270

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     271 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 330

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     331 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 390

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 450

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     451 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 510

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 570

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 630

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     631 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 690

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 750

Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     751 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 810

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     811 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 870

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     871 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 930

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaaga 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaaga 990

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     991 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1050

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1110

Qy    1081 tgtttatttg 1090
          ||||||||||
Db    1111 tgtttatttg 1120
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RESULT 7
AAF28841
ID AAF28841 standard; DNA; 1139 BP.
XX
AC AAF28841;
XX
DT 25-APR-2001 (first entry)
XX
DE Human interleukin-10 homologue IL-D110 DNA sequence.

```
XX
KW   Anti-inflammatory; immunosuppressive; cytostatic; antirheumatic; human;
KW   antiarthritic; dermatological; thyromimetic; gene therapy; inflammation;
KW   interleukin 10 homologue; IL-D110; IL-D210; cytokine; tumour therapy;
KW   haematopoietic cell; probe; immunogen; systemic lupus erythematosus;
KW   rheumatoid arthritis; Hashimoto's autoimmune response; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             59..598
FT                   /*tag= a
FT                   /product= "IL-D110"
FT                   /transl_except= (pos:245..247,aa:Xaa)
FT                   /note= "Xaa=unknown"
FT   sig_peptide     59..157
FT                   /*tag= b
FT   mat_peptide     158..595
FT                   /*tag= c
XX
PN   WO200073457-A1.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14729.
XX
PR   27-MAY-1999;   99US-0322806.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Parham CL,  De Waal Malefyt R,  Marehalli NL;
XX
DR   WPI; 2001-061539/07.
DR   P-PSDB; AAB37122.
XX
PT   New interleukin-D110 genes and polypeptides useful for treating
PT   conditions associated with abnormal physiology, particularly e.g.
PT   inflammatory or autoimmune disorders -
XX
PS   Claim 3; Page 51-52; 62pp; English.
XX
CC   This sequence represents the gene sequence for a human interleukin 10
CC   homologue IL-D110. The invention also relates to another IL-10 homologue
CC   ID-210 (AAF28842). The IL-D110 is useful for treating conditions
CC   associated with abnormal physiology or development, including
CC   inflammatory conditions, either acute or chronic. The new cytokine
CC   also plays a role in the regulation or development of haematopoietic
CC   cells, e.g. lymphoid or myeloid cells, which affect immunological
CC   responses, such as inflammation and/or autoimmune disorders. These may
CC   also be used in drug screening to identify compounds having binding
CC   affinity to or other relevant biological effects on IL-D110 functions,
CC   in anti-tumour therapy, as probes for detecting IL-D110 levels in samples
CC   from patients suspected of having an abnormal condition, e.g. autoimmune
CC   or inflammatory, in raising or screen antibodies, as immunogen, in
CC   diagnostic assays, and in detecting, isolating or identifying a DNA clone
CC   encoding IL-D110 or IL-D210 from a natural source. IL-D110 antagonists
CC   may be used to block immune responses, e.g. in situations as inflammatory
CC   or autoimmune responses, including rheumatoid arthritis, systemic lupus
CC   erythematosus, or Hashimoto's autoimmune responses.
XX
SQ   Sequence 1139 BP; 337 A; 238 C; 227 G; 333 T; 4 other;
```

```
  Query Match             83.7%;  Score 934;  DB 22;  Length 1139;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 1084;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
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Db      39 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 98

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      99 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 158

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     159 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 218

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     219 accgcaccttcatgctggctaaggaggntagcttggctgataacaacacagacgttcgtc 278

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     279 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 338

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     339 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 398

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     399 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 458

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     459 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 518

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     519 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 578

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     579 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 638

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttaaccaaaaggaagatggg 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     639 ctgctagaaataacaattagatgccccaaagcgatttttttaaccaaaaggaagatggg 698

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     699 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaaggr 758

Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     759 aaccaatgccacttttgtttataagaccagaaggtagactttctwagcatagatatttat 818

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaataa 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     819 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaataa 878

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     879 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 938

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     939 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 998

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     999 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1058

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattattatagagctataaca 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1059 ttgctacttgagtgtaaggctaatattgatatttatgacaataattattatagagctataaca 1118

Qy    1081 tgtttat 1087
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Db    1119 tgtttat 1125
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RESULT 8
AAA28839

```
ID   AAA28839 standard; cDNA; 690 BP.
XX
AC   AAA28839;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human T cell inducible factor cDNA.
XX
KW   TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW   Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;
KW   probe; chromosome 12q15; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             72..611
FT                   /*tag= a
XX
PN   WO200024758-A1.
XX
PD   04-MAY-2000.
XX
PF   18-OCT-1999;   99WO-US24424.
XX
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Dumoutier L,  Louhed J,  Renauld J;
XX
DR   WPI; 2000-422495/36.
DR   P-PSDB; AAY92879.
XX
PT   New nucleic acid molecule encoding a T cell derived inducible factor
PT   for treating asthma, an allergy or lymphoma
XX
PS   Claim 1; Page 38; 46pp; English.
XX
CC   This cDNA encodes a human T cell derived inducible factor (TIF). The gene
CC   was mapped to chromosome 12q15. The human TIF was identified based on
CC   homology to a murine TIF, which was identified by subtraction cloning
CC   from a murine lymphoma cell line BW5147 in the presence or absence of
CC   interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to
CC   add any cytokines to its culture medium. Many IL-9 activities are
CC   mediated by activation of STAT transcription factors. The novel TIFs were
CC   expressed in the presence of IL-9, but not in its absence. TIFs induce
CC   STAT activation in cells. They can be used, e.g. in the stimulation of
CC   regeneration of targeted tissues. Their inhibitors or antagonists can be
CC   used to retard, prevent or inhibit differentiation of other tissues. The
CC   TIFs and their coding sequences are useful in the treatment of asthma,
CC   allergies and lymphoma (claimed). They are also useful for identifying
CC   compounds that inhibit or activate T cell induced factor activity in a
CC   cell (claimed).
XX
SQ   Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;
```

```
  Query Match             57.3%;  Score 639;  DB 21;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 2e-301;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 291

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 351

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 411

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 471

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 531

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 591

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 651

Qy     601 ctgctagaaataacaattagatgccccaaagcgattttt 639
           |||||||||||||||||||||||||||||||||||||||
Db     652 ctgctagaaataacaattagatgccccaaagcgattttt 690
```

```
RESULT   9
AAS14875
ID   AAS14875 standard; cDNA; 690 BP.
XX
AC   AAS14875;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Human cDNA encoding T cell derived inducible factor, TIF.
XX
KW   Human; T cell derived inducible factor; TIF; ss; antiallergic;
KW   antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW   cancer; lymphoma; immune system disorder; allergy; asthma;
KW   acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW   thyroiditis; melanoma; hepatoma.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             72..611
FT                   /*tag= a
FT                   /product= "TIF"
FT                   /transl_except= (pos:159..161,aa:Glu)
FT                   /transl_except= (pos:378..380,aa:Ile)
FT                   /transl_except= (pos:405..407,aa:Arg)
FT                   /transl_except= (pos:519..521,aa:Cys)
XX
PN   US2001024652-A1.
XX
PD   27-SEP-2001.
XX
PF   29-DEC-2000; 2000US-0751797.
XX
PR   18-OCT-1999;   99US-0419568.
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (DUMO/) DUMOUTIER L.
PA   (LOUA/) LOUAHED J.
```

```
PA   (RENA/) RENAULD J.
XX
PI   Dumoutier L,  Louahed J,  Renauld J;
XX
DR   WPI; 2001-638496/73.
DR   P-PSDB; AAU09091.
XX
PT   New isolated nucleic acid molecules encoding T cell inducible factors,
PT   useful as markers for expression or effect of interleukin (IL)-9 in a
PT   subject and diagnosing susceptibility to asthma or allergy
XX
PS   Claim 1; Page 17; 26pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule, which encodes
CC   a T cell derived inducible factor (TIF) which are upregulated by the
CC   cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC   activation. The TIF proteins (or their muteins) may be used to test IL-9
CC   ant/agonists for their potency against lymphomas, immune system
CC   disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC   autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC   or inhibit differentiation of tissue types in which they are active and
CC   therefore be used to develop treatments for melanomas and hepatomas.
CC   The present sequence encodes human TIF.
XX
SQ   Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;


  Query Match             57.3%;  Score 639;  DB 22;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 2e-301;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 291

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 351

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 411

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 471

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     472 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 531

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     532 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 591

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     592 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 651

Qy     601 ctgctagaaataacaattagatgccccaaagcgattttt 639
          |||||||||||||||||||||||||||||||||||||||
Db     652 ctgctagaaataacaattagatgccccaaagcgattttt 690


RESULT  10
AAA28840
ID   AAA28840 standard; DNA; 4796 BP.
XX
AC   AAA28840;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human T cell inducible factor genomic DNA.
XX
KW   TIF; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW   Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;
KW   probe; chromosome 12q15; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             108..4717
FT                   /*tag= a
FT   exon            1..257
FT                   /*tag= b
FT   intron          258..688
FT                   /*tag= c
FT   exon            689..754
FT                   /*tag= d
FT   intron          755..870
FT                   /*tag= e
FT   exon            871..1014
FT                   /*tag= f
FT   intron          1015..1938
FT                   /*tag= g
FT   exon            1939..2004
FT                   /*tag= h
FT   intron          2005..3837
FT                   /*tag= i
FT   exon            3838..4796
FT                   /*tag= j
XX
PN   WO200024758-A1.
XX
PD   04-MAY-2000.
XX
PF   18-OCT-1999;   99WO-US24424.
XX
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Dumoutier L,  Louhed J,  Renauld J;
XX
DR   WPI; 2000-422495/36.
DR   P-PSDB; AAY92879.
XX
PT   New nucleic acid molecule encoding a T cell derived inducible factor
PT   for treating asthma, an allergy or lymphoma
XX
PS   Claim 1; Page 39-40; 46pp; English.
XX
CC   This DNA encodes a human T cell derived inducible factor (TIF). The gene
CC   was mapped to chromosome 12q15. The human TIF was identified based on
CC   homology to a murine TIF, which was identified by subtraction cloning
CC   from a murine lymphoma cell line BW5147 in the presence or absence of
CC   interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to
CC   add any cytokines to its culture medium. Many IL-9 activities are
CC   mediated by activation of STAT transcription factors. The novel TIFs were
CC   expressed in the presence of IL-9, but not in its absence. TIFs induce
CC   STAT activation in cells. They can be used, e.g. in the stimulation of
CC   regeneration of targeted tissues. Their inhibitors or antagonists can be
CC   used to retard, prevent or inhibit differentiation of other tissues. The
```

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CC   TIFs and their coding sequences are useful in the treatment of asthma,
CC   allergies and lymphoma (claimed). They are also useful for identifying
CC   compounds that inhibit or activate T cell induced factor activity in a
CC   cell (claimed).
XX
SQ   Sequence 4796 BP; 1339 A; 912 C; 1063 G; 1482 T; 0 other;


  Query Match             18.5%;  Score 207;  DB 21;  Length 4796;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-91;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggagg 207
           |||||||||||||||||||||||||||
Db     232 accgcaccttcatgctggctaaggagg 258


RESULT  11
AAS14876
ID   AAS14876 standard; DNA; 4797 BP.
XX
AC   AAS14876;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Human partial genomic DNA for T cell derived inducible factor, TIF.
XX
KW   Human; T cell derived inducible factor; TIF; ds; antiallergic;
KW   antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW   cancer; lymphoma; immune system disorder; allergy; asthma;
KW   acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW   thyroiditis; melanoma; hepatoma.
XX
OS   Homo sapiens.
XX
PN   US2001024652-A1.
XX
PD   27-SEP-2001.
XX
PF   29-DEC-2000; 2000US-0751797.
XX
PR   18-OCT-1999;   99US-0419568.
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (DUMO/) DUMOUTIER L.
PA   (LOUA/) LOUAHED J.
PA   (RENA/) RENAULD J.
XX
PI   Dumoutier L,  Louahed J,  Renauld J;
XX
DR   WPI; 2001-638496/73.
XX
PT   New isolated nucleic acid molecules encoding T cell inducible factors,
PT   useful as markers for expression or effect of interleukin (IL)-9 in a
PT   subject and diagnosing susceptibility to asthma or allergy
XX
PS   Claim 1; Page 17-19; 26pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule, which encodes
CC   a T cell derived inducible factor (TIF) which are upregulated by the
CC   cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC   activation. The TIF proteins (or their muteins) may be used to test IL-9
CC   ant/agonists for their potency against lymphomas, immune system
CC   disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC   autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC   or inhibit differentiation of tissue types in which they are active and
CC   therefore be used to develop treatments for melanomas and hepatomas.
CC   The present sequence a partial genomic sequence for Human TIF.
XX
SQ   Sequence 4797 BP; 1339 A; 910 C; 1063 G; 1485 T; 0 other;


  Query Match             18.5%;  Score 207;  DB 22;  Length 4797;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-91;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggagg 207
           |||||||||||||||||||||||||||
Db     232 accgcaccttcatgctggctaaggagg 258


RESULT  12
AAD09746
ID   AAD09746 standard; cDNA; 778 BP.
XX
AC   AAD09746;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Mouse ZCYTO18 cDNA.
XX
KW   Mouse; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW   cancer; inflammation; gene therapy; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             47..586
FT                   /*tag= a
FT                   /product= "Mouse ZCYTO18 protein"
FT   sig_peptide     47..145
FT                   /*tag= b
FT   mat_peptide     146..583
FT                   /*tag= c
FT                   /product= "Mouse mature ZCYTO18 protein"
XX
PN   WO200146422-A1.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US35308.
XX
PR   23-DEC-1999;   99US-0471767.
PR   01-DEC-2000; 2000US-0250841.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Kindsvogel W;
XX
DR   WPI; 2001-408648/43.
DR   P-PSDB; AAE05052.
```

```
XX
PT   Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS   Example 5; Page 160-162; 167pp; English.
XX
CC   The patent discloses novel human cytokine, ZCYTO18 protein and its
CC   corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC   expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC   in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC   abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC   for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC   killing cancer cells. It is useful for increasing platelets in a
CC   patient or injured tissue. It is also used in gene therapy.
CC   The present sequence is a cDNA encoding mouse cytokine, ZCYTO18.
XX
SQ   Sequence 778 BP; 213 A; 193 C; 197 G; 175 T; 0 other;


  Query Match             3.1%;  Score 35;  DB 22;  Length 778;
  Best Local Similarity   100.0%;  Pred. No. 7e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     471 acagtgaaaaagcttggagagagtggagagatcaa 505
           |||||||||||||||||||||||||||||||||||
Db     497 acagtgaaaaagcttggagagagtggagagatcaa 531


RESULT  13
AAA28815
ID   AAA28815 standard; cDNA; 1119 BP.
XX
AC   AAA28815;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Murine T cell inducible factor alpha cDNA.
XX
KW   TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW   Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             52..591
FT                   /*tag=  a
XX
PN   WO200024758-A1.
XX
PD   04-MAY-2000.
XX
PF   18-OCT-1999;   99WO-US24424.
XX
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Dumoutier L,  Louhed J,  Renauld J;
XX
DR   WPI; 2000-422495/36.
DR   P-PSDB; AAY92877.
XX
PT   New nucleic acid molecule encoding a T cell derived inducible factor
PT   for treating asthma, an allergy or lymphoma
XX
PS   Claim 1; Page 33; 46pp; English.
XX
CC   This cDNA encodes T cell derived inducible factor (TIF) alpha identified
CC   by subtraction cloning from a murine lymphoma cell line BW5147 in the
CC   presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
CC   vitro, without the need to add any cytokines to its culture medium. Many
CC   IL-9 activities are mediated by activation of STAT transcription
CC   factors. The novel TIFs were expressed in the presence of IL-9, but not
CC   in its absence. TIFs induce STAT activation in cells. They can be used,
CC   e.g. in the stimulation of regeneration of targeted tissues. Their
CC   inhibitors or antagonists can be used to retard, prevent or inhibit
CC   differentiation of other tissues. The TIFs and their coding sequences are
CC   useful in the treatment of asthma, allergies and lymphoma (claimed). They
CC   are also useful for identifying compounds that inhibit or activate T cell
CC   induced factor activity in a cell (claimed).
XX
SQ   Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;


  Query Match             3.1%;  Score 35;  DB 21;  Length 1119;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     471 acagtgaaaaagcttggagagagtggagagatcaa 505
           |||||||||||||||||||||||||||||||||||
Db     502 acagtgaaaaagcttggagagagtggagagatcaa 536


RESULT  14
AAS14858
ID   AAS14858 standard; cDNA; 1119 BP.
XX
AC   AAS14858;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Mouse cDNA encodingT cell derived inducible factor, TIFalpha.
XX
KW   Mouse; T cell derived inducible factor; TIFalpha; ss; antiallergic;
KW   antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW   cancer; lymphoma; immune system disorder; allergy; asthma;
KW   acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW   thyroiditis; melanoma; hepatoma.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
FT                   /product= "TIFalpha"
FT   primer_bind     106..126
FT                   /*tag=  b
FT                   /note= "PCR primer appearing as AAS14861"
FT   primer_bind     complement (764..784)
FT                   /*tag=  c
FT                   /note= "PCR primer appearing as AAS14862"
XX
PN   US2001024652-A1.
XX
PD   27-SEP-2001.
XX
PF   29-DEC-2000; 2000US-0751797.
XX
PR   18-OCT-1999;   99US-0419568.
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (DUMO/) DUMOUTIER L.
PA   (LOUA/) LOUAHED J.
PA   (RENA/) RENAULD J.
XX
PI   Dumoutier L,  Louahed J,  Renauld J;
XX
DR   WPI; 2001-638496/73.
DR   P-PSDB; AAU09090.
XX
PT   New isolated nucleic acid molecules encoding T cell inducible factors,
PT   useful as markers for expression or effect of interleukin (IL)-9 in a
PT   subject and diagnosing susceptibility to asthma or allergy -
XX
PS   Claim 1; Page 10; 26pp; English.
```

XX
CC The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their muteins) may be used to test IL-9
CC ant/agonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence encodes mouse TIFalpha.
XX
SQ Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;

Query Match 3.1%; Score 35; DB 22; Length 1119;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 acagtgaaaaagcttggagagagtggagagatcaa 505
||||||||||||||||||||||||||||||||||||
Db 502 acagtgaaaaagcttggagagagtggagagatcaa 536

RESULT 15
AAC81774
ID AAC81774 standard; cDNA; 1166 BP.
XX
AC AAC81774;
XX
DT 23-FEB-2001 (first entry)
XX
DE Murine GIL-19 protein coding sequence.
XX
KW Mouse; GIL-19/AE289; IL-10; interleukin-10; nutrition;
KW cell proliferation; immune stimulation; immune suppression;
KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.
XX
OS Mus sp.
XX
PN WO200065027-A2.
XX
PD 02-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11479.
XX
PR 28-APR-1999; 99US-0131473.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Fouser L, Spaulding V, Xuan D;
XX
DR WPI; 2000-687325/67.
XX
PT Human GIL-19 protein that shows a high degree of homology to IL
PT (interleukin)-10, useful in upregulation of humoral immune responses,
PT as an antiinflammatory agent and as a modulator of immune responses
PT associated with injury -
XX
PS Disclosure; Fig 1; 60pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC novel human GIL-19/AE289 protein. The protein shows homology to
CC interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used
CC in the regulation of cell proliferation and differentiation,
CC haematopoiesis, immune stimulation or suppression, tissue growth and
CC tumour inhibition. In addition, it also has uses in the treatment of
CC inflammation and in nutrition.
XX
SQ Sequence 1166 BP; 375 A; 241 C; 244 G; 306 T; 0 other;

Query Match 3.1%; Score 35; DB 21; Length 1166;
Best Local Similarity 100.0%; Pred. No. 7.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 acagtgaaaaagcttggagagagtggagagatcaa 505
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Db 525 acagtgaaaaagcttggagagagtggagagatcaa 559

Search completed: September 23, 2002, 02:11:28
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:51:20 ; Search time 51.77 Seconds
(without alignments)
5295.093 Million cell updates/sec

Title: US-09-746-375-1
Perfect score: 1116
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttggatatccta 1116

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 14

Total number of hits satisfying chosen parameters: 1870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	639	57.3	690	4	US-09-354-243B-24	Sequence 24, Appl
	2	207	18.5	4797	4	US-09-354-243B-25	Sequence 25, Appl
	3	35	3.1	1119	4	US-09-178-973B-7	Sequence 7, Appli
	4	35	3.1	1119	4	US-09-354-243B-7	Sequence 7, Appli
	5	31	2.8	7445	4	US-09-178-973B-8	Sequence 8, Appli
	6	31	2.8	7445	4	US-09-354-243B-8	Sequence 8, Appli
	7	28	2.5	1111	4	US-09-178-973B-9	Sequence 9, Appli
	8	28	2.5	1111	4	US-09-354-243B-9	Sequence 9, Appli
	9	28	2.5	5935	4	US-09-178-973B-17	Sequence 17, Appl
	10	28	2.5	5935	4	US-09-354-243B-29	Sequence 29, Appl
c	11	22	2.0	22	4	US-09-354-243B-16	Sequence 16, Appl
c	12	21	1.9	21	4	US-09-354-243B-18	Sequence 18, Appl
c	13	21	1.9	21	4	US-09-354-243B-19	Sequence 19, Appl
	14	20	1.8	2908	3	US-08-487-799-1	Sequence 1, Appli
	15	20	1.8	22846	2	US-08-469-461-3	Sequence 3, Appli
	16	20	1.8	22846	3	US-07-890-609-3	Sequence 3, Appli
	17	18	1.6	1939	1	US-07-715-751B-2	Sequence 2, Appli
c	18	17	1.5	356	4	US-09-319-730-16	Sequence 16, Appl
c	19	17	1.5	452	2	US-08-378-235B-4	Sequence 4, Appli
	20	17	1.5	573	2	US-08-290-665A-134	Sequence 134, App
	21	17	1.5	573	5	PCT-US95-10398-134	Sequence 134, App
c	22	17	1.5	1519	1	US-07-971-759-19	Sequence 19, Appl
c	23	17	1.5	1628	2	US-08-883-515-3	Sequence 3, Appli
	24	17	1.5	3217	4	US-09-232-200-64	Sequence 64, Appl
	25	17	1.5	3217	4	US-09-232-197-64	Sequence 64, Appl
	26	17	1.5	3217	4	US-09-232-201-64	Sequence 64, Appl
	27	17	1.5	9620	4	US-08-952-127-11	Sequence 11, Appl
	28	17	1.5	15378	3	US-08-785-420-1	Sequence 1, Appli
c	29	17	1.5	28804	2	US-08-592-874-1	Sequence 1, Appli
c	30	17	1.5	28804	3	US-09-096-942-2	Sequence 2, Appli
c	31	17	1.5	28804	3	US-09-096-867-2	Sequence 2, Appli
	32	17	1.5	80161	3	US-09-036-987A-1	Sequence 1, Appli
	33	17	1.5	80161	4	US-09-370-700-1	Sequence 1, Appli
c	34	17	1.5	246240	2	US-08-724-394A-20	Sequence 20, Appl
c	35	17	1.5	246240	2	US-08-724-394A-21	Sequence 21, Appl
c	36	17	1.5	246240	2	US-08-724-394A-22	Sequence 22, Appl
	37	16	1.4	77	1	US-08-400-440A-30	Sequence 30, Appl
	38	16	1.4	77	1	US-08-463-093A-30	Sequence 30, Appl
	39	16	1.4	77	2	US-08-460-888A-30	Sequence 30, Appl
	40	16	1.4	77	2	US-08-894-578-30	Sequence 30, Appl
	41	16	1.4	77	4	US-09-412-017-30	Sequence 30, Appl
c	42	16	1.4	86	2	US-08-525-742-50	Sequence 50, Appl
	43	16	1.4	201	1	US-08-021-667A-18	Sequence 18, Appl
	44	16	1.4	201	1	US-08-410-544-18	Sequence 18, Appl
	45	16	1.4	201	1	US-08-728-785A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-354-243B-24
; Sequence 24, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (TIFs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-24

Query Match 57.3%; Score 639; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 5e-302;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 291

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 351

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 471

Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 531

Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    532 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 591

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
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Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttt 639
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Db    652 ctgctagaaataacaattagatgccccaaagcgatttttt 690


RESULT   2
US-09-354-243B-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 25
;   LENGTH: 4797
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-25


  Query Match             18.5%;  Score 207;  DB 4;  Length 4797;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-91;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
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Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy    181 accgcaccttcatgctggctaaggagg 207
          |||||||||||||||||||||||||||
Db    232 accgcaccttcatgctggctaaggagg 258


RESULT   3
US-09-178-973B-7
; Sequence 7, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 7
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-7


  Query Match             3.1%;  Score 35;  DB 4;  Length 1119;
  Best Local Similarity   100.0%;  Pred. No. 1e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    471 acagtgaaaaagcttggagagagtggagagatcaa 505
          |||||||||||||||||||||||||||||||||||
Db    502 acagtgaaaaagcttggagagagtggagagatcaa 536


RESULT   4
US-09-354-243B-7
; Sequence 7, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 7
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
US-09-354-243B-7


  Query Match             3.1%;  Score 35;  DB 4;  Length 1119;
  Best Local Similarity   100.0%;  Pred. No. 1e-07;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    471 acagtgaaaaagcttggagagagtggagagatcaa 505
          |||||||||||||||||||||||||||||||||||
Db    502 acagtgaaaaagcttggagagagtggagagatcaa 536


RESULT   5
US-09-178-973B-8
; Sequence 8, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
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;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
;   LENGTH: 7445
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-8


  Query Match             2.8%;  Score 31;  DB 4;  Length 7445;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-06;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaacat 1011
          |||||||||||||||||||||||||||||||
Db   7008 tttattaatatggatttatttatagaaacat 7038


RESULT   6
US-09-354-243B-8
; Sequence 8, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 8
;   LENGTH: 7445
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
US-09-354-243B-8


  Query Match             2.8%;  Score 31;  DB 4;  Length 7445;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-06;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaacat 1011
          |||||||||||||||||||||||||||||||
Db   7008 tttattaatatggatttatttatagaaacat 7038


RESULT   7
US-09-178-973B-9
; Sequence 9, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
;   LENGTH: 1111
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-9


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  Best Local Similarity   100.0%;  Pred. No. 0.00026;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaa 1008
          ||||||||||||||||||||||||||||
Db    981 tttattaatatggatttatttatagaaa 1008


RESULT   8
US-09-354-243B-9
; Sequence 9, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 9
;   LENGTH: 1111
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
US-09-354-243B-9


  Query Match             2.5%;  Score 28;  DB 4;  Length 1111;
  Best Local Similarity   100.0%;  Pred. No. 0.00026;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaa 1008
          ||||||||||||||||||||||||||||
Db    981 tttattaatatggatttatttatagaaa 1008


RESULT   9
US-09-178-973B-17
; Sequence 17, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
;   LENGTH: 5935
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-17


  Query Match             2.5%;  Score 28;  DB 4;  Length 5935;
  Best Local Similarity   100.0%;  Pred. No. 0.00026;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaa 1008
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Db    5694 tttattaatatggatttatttatagaaa 5721


RESULT  10
US-09-354-243B-29
; Sequence 29, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 29
;   LENGTH: 5935
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-29


  Query Match             2.5%;  Score 28;  DB 4;  Length 5935;
  Best Local Similarity   100.0%;  Pred. No. 0.00026;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaa 1008
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Db   5694 tttattaatatggatttatttatagaaa 5721


RESULT  11
US-09-354-243B-16/c
; Sequence 16, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 16
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-16


  Query Match             2.0%;  Score 22;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.22;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    475 tgaaaaagcttggagagagtgg 496
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Db     22 TGAAAAAGCTTGGAGAGAGTGG 1


RESULT  12
US-09-354-243B-18/c
; Sequence 18, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 18
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-18


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  Best Local Similarity   100.0%;  Pred. No. 0.67;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    370 aggtggtgcccttcctggcca 390
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Db     21 AGGTGGTGCCCTTCCTGGCCA 1


RESULT  13
US-09-354-243B-19/c
; Sequence 19, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 19
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-19


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Qy    370 aggtggtgcccttcctggcca 390
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RESULT  14
US-08-487-799-1
; Sequence 1, Application US/08487799C
; Patent No. 6010908
; GENERAL INFORMATION:
;  APPLICANT: Gruenert, Deiter C.
```

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;  APPLICANT: Kunzelmann, Karl
;  TITLE OF INVENTION: GENE THERAPY BY SMALL FRAGMENTS HOMOLOGOUS REPLACEMENT
;  FILE REFERENCE: 480.18-1(HV)
;  CURRENT APPLICATION NUMBER: US/08/487,799C
;  CURRENT FILING DATE: 1995-06-07
;  EARLIER APPLICATION NUMBER: 07/933,471
;  EARLIER FILING DATE: 1992-08-21
;  EARLIER APPLICATION NUMBER: 08/409,544
;  EARLIER FILING DATE: 1995-03-24
;  NUMBER OF SEQ ID NOS: 87
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2908
;   TYPE: DNA
;   ORGANISM: human
US-08-487-799-1


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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps.    0;

Qy     822 caatttatttttaaataat 841
           ||||||||||||||||||||
Db    1453 caatttatttttaaataat 1472


RESULT  15
US-08-469-461-3
; Sequence 3, Application US/08469461B
; Patent No. 5981178
; GENERAL INFORMATION:
;  APPLICANT: Tsui, Lap-Chee
;  APPLICANT: Rommins, Johanna M.
;  APPLICANT: Kerem, Bat-Sheva
;  TITLE OF INVENTION: Introns and Exons of the Cystic Fibrosis Gene and
;  TITLE OF INVENTION: Mutations at Various Positions of the Gene
;  FILE REFERENCE: 3477-61, 033477/139840
;  CURRENT APPLICATION NUMBER: US/08/469,461B
;  CURRENT FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 22846
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-469-461-3


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Qy     822 caatttatttttaaataat 841
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Db    9242 caatttatttttaaataat 9261


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Job time: 7111 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:42:04 ; Search time 1730.87 Seconds
(without alignments)
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 14

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	66	5.9	389	12	AQ104025	AQ104025 HS_3108_B
2	28	2.5	256	9	AV030414	AV030414 AV030414
3	28	2.5	700	11	AK005228	AK005228 Mus muscu
4	23	2.1	116	10	BI314237	BI314237 dai33c12.
c 5	22	2.0	381	10	BI341427	BI341427 368848 MA
c 6	22	2.0	431	10	BI341431	BI341431 368853 MA
c 7	22	2.0	446	12	AZ167394	AZ167394 SP_0098_A
8	22	2.0	718	12	AQ780852	AQ780852 HS_3113_B
c 9	21	1.9	182	10	W21516	W21516 zb51e10.r1
c 10	21	1.9	192	10	W21016	W21016 zb50f12.r1
c 11	21	1.9	210	9	AA341708	AA341708 EST47366
c 12	21	1.9	234	9	AA334932	AA334932 EST39303
13	21	1.9	240	9	AW486359	AW486359 72999 MAR
c 14	21	1.9	251	10	W05048	W05048 za78g02.r1
c 15	21	1.9	262	9	AA331022	AA331022 EST34794
16	21	1.9	295	9	AV097026	AV097026 AV097026
c 17	21	1.9	301	10	BF827895	BF827895 RC0-HN002
c 18	21	1.9	304	10	F00991	F00991 HSB89H092 S
19	21	1.9	305	9	AW486360	AW486360 73004 MAR
c 20	21	1.9	315	9	AA346165	AA346165 EST52274
c 21	21	1.9	327	10	BF827890	BF827890 RC0-HN002
c 22	21	1.9	335	9	AA328929	AA328929 EST32477
c 23	21	1.9	378	9	AA112190	AA112190 zn60d07.r
c 24	21	1.9	384	12	AZ223713	AZ223713 RPCI-23-5
c 25	21	1.9	391	9	AA180126	AA180126 zp34c02.r
c 26	21	1.9	401	9	AA194504	AA194504 zq06f07.r
c 27	21	1.9	401	9	AA346264	AA346264 EST52401
28	21	1.9	422	10	BM276287	BM276287 PfESToaa7
c 29	21	1.9	429	10	W88590	W88590 zh70h12.r1
c 30	21	1.9	433	9	AA192403	AA192403 zq01a01.r
c 31	21	1.9	458	9	AA182400	AA182400 zp36g01.r
c 32	21	1.9	464	9	AA196108	AA196108 zp99e07.r
33	21	1.9	473	10	BM276043	BM276043 PfESToaa6
c 34	21	1.9	476	12	AQ203627	AQ203627 HS_3103_B
35	21	1.9	478	12	AQ664172	AQ664172 HS_5493_B
36	21	1.9	479	9	AW104304	AW104304 xd77a10.x
c 37	21	1.9	480	10	W93616	W93616 zd95c04.r1
c 38	21	1.9	503	12	AZ478642	AZ478642 1M0298C23
c 39	21	1.9	507	12	AQ992968	AQ992968 RPCI-23-3
c 40	21	1.9	529	10	BI816005	BI816005 PfESToaa3
41	21	1.9	545	10	BM276174	BM276174 PfESToaa7
42	21	1.9	548	10	BM275812	BM275812 PfESToaa8
43	21	1.9	549	10	BM275687	BM275687 PfESToaa5
44	21	1.9	551	10	BM275051	BM275051 PfESToaa7
45	21	1.9	555	10	BM274386	BM274386 PfESToaa4

ALIGNMENTS

RESULT 1
AQ104025/c
LOCUS AQ104025 389 bp DNA linear GSS 28-AUG-1998
DEFINITION HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.
ACCESSION AQ104025
VERSION AQ104025.1 GI:3478961
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 389)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3108 row: F column: 1
Class: BAC ends
High quality sequence stop: 389.
FEATURES Location/Qualifiers
source 1. .389
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 2.5e-21;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    417 catattgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtg 476
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Db    144 CATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTG 85

Qy    477 aaaaag 482
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Db     84 AAAAAG 79


RESULT   2
AV030414
LOCUS       AV030414                 256 bp    mRNA    linear   EST 31-AUG-1999
DEFINITION  AV030414 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA
            clone 1500012D04, mRNA sequence.
ACCESSION   AV030414
VERSION     AV030414.1  GI:4829962
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="1500012D04"
                     /clone_lib="Mus musculus adult C57BL/6J cerebellum"
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                     /tissue_type="cerebellum"
                     /dev_stage="adult"
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ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.014;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaa 1008
          ||||||||||||||||||||||||||||
Db    131 TTTATTAATATGGATTTATTTATAGAAA 158


RESULT   3
AK005228
LOCUS       AK005228                 700 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
            library, clone:1500012D04:interleukin 10-related T cell-derived
            inducible factor, full insert sequence.
ACCESSION   AK005228
VERSION     AK005228.1  GI:12837639
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:1500012D04.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2  (sites)
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3  (sites)
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 700)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
```

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            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence[5'
            GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA
            was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3'
            end: SstI. Host: SOLR.
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                      /tissue_type="cerebellum"
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                      evidence:ISS
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BASE COUNT      255 a    105 c    133 g    207 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.012;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    981 tttattaatatggatttatttatagaaa 1008
          ||||||||||||||||||||||||||||
Db    572 TTTATTAATATGGATTTATTTATAGAAA 599


RESULT   4
BI314237
LOCUS       BI314237                116 bp    mRNA    linear   EST 20-JUL-2001
DEFINITION  dai33c12.x1 NICHD XGC Sp1 Xenopus laevis cDNA clone IMAGE:4963582
            3', mRNA sequence.
ACCESSION   BI314237
VERSION     BI314237.1  GI:14988564
KEYWORDS    EST.
SOURCE      African clawed frog.
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 116)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:8355"
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                      /clone_lib="NICHD XGC Sp1"
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                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: spleen; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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BASE COUNT       36 a     17 c     13 g     50 t
ORIGIN


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Qy    934 ataaatgtatttattattattat 956
          |||||||||||||||||||||||
Db      5 ATAAATGTATTTATTATTATTAT 27


RESULT   5
BI341427/c
LOCUS       BI341427                381 bp    mRNA    linear   EST 30-JUL-2001
DEFINITION  368848 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI341427
VERSION     BI341427.1  GI:15034716
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 381)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 108  row: D  column: 15
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .381
                      /organism="Sus scrofa"
                      /db_xref="taxon:9823"
                      /clone_lib="MARC 2PIG"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                      Library made from pooled tissue from testis, ovary,
                      endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      157 a     42 c     68 g    114 t
ORIGIN


  Query Match             2.0%;  Score 22;  DB 10;  Length 381;
  Best Local Similarity   100.0%;  Pred. No. 12;
```

```
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    829 ttttttaaataattgtcttttt 850
          ||||||||||||||||||||||
Db     29 TTTTTTAAATAATTGTCTTTTT 8


RESULT   6
BI341431/c
LOCUS       BI341431                431 bp    mRNA    linear   EST 30-JUL-2001
DEFINITION  368853 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI341431
VERSION     BI341431.1  GI:15034720
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 431)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 108  row: E  column: 14
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .431
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      177 a     51 c     93 g    109 t      1 others
ORIGIN


  Query Match             2.0%;  Score 22;  DB 10;  Length 431;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    829 ttttttaaataattgtcttttt 850
          ||||||||||||||||||||||
Db    239 TTTTTTAAATAATTGTCTTTTT 218


RESULT   7
AZ167394/c
LOCUS       AZ167394                446 bp    DNA     linear   GSS 29-AUG-2000
DEFINITION  SP_0098_A2_A12_SP6E Strongylocentrotus purpuratus, purple sea
            urchin, sperm genomic BAC library Strongylocentrotus purpuratus
            genomic clone Plate=98 Col=24 Row=A, DNA sequence.
ACCESSION   AZ167394
VERSION     AZ167394.1  GI:8337762
KEYWORDS    GSS.
SOURCE      Strongylocentrotus purpuratus.
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
            Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
            ,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
            Hood,L.
  TITLE     A sea urchin genome project: Sequence scan, virtual map, and
            additional resources
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
  MEDLINE   20402566
COMMENT     Contact: Cameron, RA, Davidson, EH, Hood, L
            Division of Biology 156-29
            California Institute of Technology
            Pasadena California 91125, USA
            Tel: (626) 395-8421
            Fax: (626) 793-3047
            Email: acameron@caltech.edu
            Plate: 98  row: A  column: 24
            Seq primer: SP6
            Class: BAC ends
            High quality sequence stop: 446.
FEATURES             Location/Qualifiers
     source          1. .446
                     /organism="Strongylocentrotus purpuratus"
                     /db_xref="taxon:7668"
                     /clone="Plate=98 Col=24 Row=A"
                     /clone_lib="Strongylocentrotus purpuratus, purple sea
                     urchin, sperm genomic BAC library"
                     /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                     DH10B"
BASE COUNT      169 a     89 c     92 g     96 t
ORIGIN


  Query Match             2.0%;  Score 22;  DB 12;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    929 tatttataaatgtatttattat 950
          ||||||||||||||||||||||
Db    143 TATTTATAAATGTATTTATTAT 122


RESULT   8
AQ780852
LOCUS       AQ780852                718 bp    DNA     linear   GSS 02-AUG-1999
DEFINITION  HS_3113_B1_B02_T7C CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3113 Col=3 Row=D, DNA sequence.
ACCESSION   AQ780852
VERSION     AQ780852.1  GI:5683812
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
```

```
            BAC end Web Server: http://www.htsc.washington.edu
            Plate: 3113  row: D  column: 3
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 718.
FEATURES              Location/Qualifiers
     source           1. .718
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="Plate=3113 Col=3 Row=D"
                      /clone_lib="CIT Approved Human Genomic Sperm Library D"
                      /sex="male"
                      /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                      E-Coli DH10B"
BASE COUNT      201 a    161 c    150 g    204 t      2 others
ORIGIN


  Query Match             2.0%;  Score 22;  DB 12;  Length 718;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    776 tttattgataacatttcattgt 797
          ||||||||||||||||||||||
Db     87 TTTATTGATAACATTTCATTGT 108


RESULT   9
W21516/c
LOCUS       W21516                   182 bp    mRNA    linear   EST 20-AUG-1996
DEFINITION  zb51e10.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:307146 5' similar to gb:Z15030_rna1 MYOSIN REGULATORY LIGHT
            CHAIN 2, VENTRICULAR (HUMAN);, mRNA sequence.
ACCESSION   W21516
VERSION     W21516.1  GI:1298157
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 182)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 658   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 168.
FEATURES              Location/Qualifiers
     source           1. .182
                      /organism="Homo sapiens"
                      /db_xref="GDB:1250558"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:307146"
                      /clone_lib="Soares_fetal_lung_NbHL19W"
                      /dev_stage="19 weeks"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTTT-3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library went through one round of
                      normalization to a Cot = 5. Library constructed by Bento
                      Soares and M.Fatima Bonaldo. This library was constructed
                      from the same fetus as the fetal heart library, Soares
                      fetal heart NbHH19W."
BASE COUNT      51 a     47 c     52 g     30 t      2 others
ORIGIN


  Query Match             1.9%;  Score 21;  DB 10;  Length 182;
  Best Local Similarity   100.0%;  Pred. No. 41;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     82 tccttctcttggccctcttgg 102
          |||||||||||||||||||||
Db     34 TCCTTCTCTTGGCCCTCTTGG 14


RESULT  10
W21016/c
LOCUS       W21016                   192 bp    mRNA    linear   EST 20-AUG-1996
DEFINITION  zb50f12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:307055 5' similar to gb:L03785 MYOSIN REGULATORY LIGHT CHAIN
            5 (HUMAN);, mRNA sequence.
ACCESSION   W21016
VERSION     W21016.1  GI:1297912
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 192)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 685   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 166.
FEATURES              Location/Qualifiers
     source           1. .192
                      /organism="Homo sapiens"
                      /db_xref="GDB:1250467"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:307055"
                      /clone_lib="Soares_fetal_lung_NbHL19W"
                      /dev_stage="19 weeks"
                      /lab_host="DH10B (ampicillin resistant)"
                      /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                      modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                      strand cDNA was primed with a Not I - oligo(dT) primer
                      [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTTT-3'],
                      double-stranded cDNA was size selected, ligated to Eco RI
                      adapters (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of a modified pT7T3 vector
                      (Pharmacia). Library went through one round of
```

normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHH19W."
BASE COUNT 53 a 53 c 51 g 34 t 1 others
ORIGIN

Query Match 1.9%; Score 21; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 tccttctcttggccctcttgg 102
||||||||||||||||||||
Db 59 TCCTTCTCTTGGCCCTCTTGG 39

RESULT 11
AA341708/c
LOCUS AA341708 210 bp mRNA linear EST 21-APR-1997
DEFINITION EST47366 Fetal muscle Homo sapiens cDNA 5' end similar to similar to myosin light chain 2, mRNA sequence.
ACCESSION AA341708
VERSION AA341708.1 GI:1994173
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 210)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .210
/organism="Homo sapiens"
/db_xref="ATCC (inhost):143553"
/db_xref="taxon:9606"
/clone_lib="Fetal muscle"
/tissue_type="muscle"
/dev_stage="fetus, 24 wks"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 55 a 56 c 61 g 34 t 4 others
ORIGIN

Query Match 1.9%; Score 21; DB 9; Length 210;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 tccttctcttggccctcttgg 102
||||||||||||||||||||
Db 62 TCCTTCTCTTGGCCCTCTTGG 42

RESULT 12
AA334932/c
LOCUS AA334932 234 bp mRNA linear EST 21-APR-1997
DEFINITION EST39303 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to Myosin light chain-2, type I, mRNA sequence.
ACCESSION AA334932
VERSION AA334932.1 GI:1987250
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 234)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES Location/Qualifiers
source 1. .234
/organism="Homo sapiens"
/db_xref="ATCC (inhost):136696"
/db_xref="taxon:9606"
/clone_lib="Embryo, 9 week"
/dev_stage="embryo, 9 wks"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 62 a 62 c 69 g 39 t 2 others
ORIGIN

Query Match 1.9%; Score 21; DB 9; Length 234;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      82 tccttctcttggccctcttgg 102
           ||||||||||||||||||||
Db      61 TCCTTCTCTTGGCCCTCTTGG 41


RESULT  13
AW486359
LOCUS       AW486359                 240 bp    mRNA    linear   EST 25-APR-2001
DEFINITION  72999 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW486359
VERSION     AW486359.1  GI:7056465
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 240)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 33  row: G  column: 10
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .240
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."
BASE COUNT       60 a     39 c     33 g    108 t
ORIGIN


  Query Match             1.9%;  Score 21;  DB 9;  Length 240;
  Best Local Similarity   100.0%;  Pred. No. 40;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     934 ataaatgtatttattattatt 954
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Db      30 ATAAATGTATTTATTATTATT 50


RESULT  14
W05048/c
LOCUS       W05048                   251 bp    mRNA    linear   EST 23-APR-1996
DEFINITION  za78g02.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone
            IMAGE:298706 5' similar to gb:Z15030_rna1 MYOSIN REGULATORY LIGHT
            CHAIN 2, VENTRICULAR (HUMAN);, mRNA sequence.
ACCESSION   W05048
VERSION     W05048.1  GI:1277978
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 251)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 176.
FEATURES             Location/Qualifiers
     source          1. .251
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:298706"
                     /clone_lib="Soares_fetal_lung_NbHL19W"
                     /dev_stage="19 weeks"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: lung; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer
                     [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCAATTTTTTTTTTTTTTTT-3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. This library was constructed
                     from the same fetus as the fetal heart library, Soares
                     fetal heart NbHH19W."
BASE COUNT       72 a     59 c     70 g     45 t      5 others
ORIGIN


  Query Match             1.9%;  Score 21;  DB 10;  Length 251;
  Best Local Similarity   100.0%;  Pred. No. 39;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      43 TCCTTCTCTTGGCCCTCTTGG 23


RESULT  15
AA331022/c
LOCUS       AA331022                 262 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST34794 Embryo, 6 week I Homo sapiens cDNA 5' end similar to
            similar to myosin 2, light chain, type I, mRNA sequence.
ACCESSION   AA331022
VERSION     AA331022.1  GI:1983264
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 262)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
            Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
```

,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.

FEATURES Location/Qualifiers
source 1. .262
/organism="Homo sapiens"
/db_xref="ATCC (inhost):132654"
/db_xref="taxon:9606"
/clone_lib="Embryo, 6 week I"
/dev_stage="embryo, 6 wks"
/note="Organ: embryo; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 70 a 68 c 73 g 50 t 1 others

ORIGIN

Query Match 1.9%; Score 21; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      29 TCCTTCTCTTGGCCCTCTTGG 9
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Search completed: September 23, 2002, 02:07:33
Job time: 5129 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:31:39 ; Search time 2227.14 Seconds
(without alignments)
10486.101 Million cell updates/sec

Title: US-09-746-375-1
Perfect score: 1116
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttggatatccta 1116

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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8: gb_pl:*
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10: gb_ro:*
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12: gb_sy:*
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14: gb_vi:*
15: em_ba:*
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17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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25: em_pl:*
26: em_ro:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	1116	100.0	1116	6	AX151713	AX151713 Sequence
2	1116	100.0	1116	6	AX179578	AX179578 Sequence
3	1114.4	99.9	1167	9	AF279437	AF279437 Homo sapi
4	1114	99.8	1152	6	AX092422	AX092422 Sequence
5	1096.6	98.3	1139	6	AX054620	AX054620 Sequence
6	1090.4	97.7	1132	6	AX048204	AX048204 Sequence
7	639	57.3	690	9	HSA277247	AJ277247 Homo sapi
8	636.4	57.0	8393	9	AF387519	AF387519 Homo sapi
c 9	636.4	57.0	133350	9	AC022511	AC022511 Homo sapi
c 10	636.4	57.0	191111	9	AC007458	AC007458 Homo sapi
11	564	50.5	135146	2	AC087562	AC087562 Pan trogl
12	525.2	47.1	1111	6	AR165228	AR165228 Sequence
13	525.2	47.1	1118	10	MMU249492	AJ249492 Mus muscu
14	524.4	47.0	1119	6	AR165226	AR165226 Sequence
15	524.4	47.0	1121	10	MMU249491	AJ249491 Mus muscu
16	429.2	38.5	778	6	AX179614	AX179614 Sequence
17	380	34.1	537	6	AX054622	AX054622 Sequence
18	356.4	31.9	501	6	AX179581	AX179581 Sequence
19	216.4	19.4	5935	6	AR165234	AR165234 Sequence
20	216.4	19.4	5935	10	MMU294728	AJ294728 Mus muscu
21	215.6	19.3	7445	6	AR165227	AR165227 Sequence
22	215.6	19.3	8270	10	MMU294727	AJ294727 Mus muscu
23	207	18.5	5397	9	HSA277248	AJ277248 Homo sapi
24	73.2	6.6	194074	9	AC090095	AC090095 Homo sapi
25	73.2	6.6	199810	9	AC018443	AC018443 Homo sapi
26	73	6.5	175959	2	AL450429	AL450429 Homo sapi
c 27	72	6.5	213056	9	AC103590	AC103590 Homo sapi
c 28	72	6.5	213080	30	AL357933	AL357933 Human DNA
c 29	71.6	6.4	189662	9	AC015468	AC015468 Homo sapi
c 30	71.4	6.4	198405	2	AC104317	AC104317 Homo sapi
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33	70.4	6.3	152637	2	AC006734	AC006734 Caenorhab
c 34	69.8	6.3	151938	9	HS323M4	AL033378 Human DNA
35	69.8	6.3	199392	2	AC090192	AC090192 Homo sapi
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c 38	69.4	6.2	177164	9	AL365202	AL365202 Human DNA
c 39	69.2	6.2	92148	2	AC098159	AC098159 Rattus no
c 40	69.2	6.2	200306	2	AC104826	AC104826 Homo sapi
c 41	69	6.2	201312	2	AC067900	AC067900 Homo sapi
c 42	68.8	6.2	198692	2	AC090530	AC090530 Homo sapi
c 43	67.8	6.1	168272	2	AC092451	AC092451 Homo sapi
c 44	67.6	6.1	150153	2	AC091869	AC091869 Homo sapi
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ALIGNMENTS

RESULT 1
AX151713
LOCUS AX151713 1116 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 14 from Patent WO0140467.
ACCESSION AX151713
VERSION AX151713.1 GI:14533647
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Presnell,S.R., Xu,W., Kindsvogel,W. and Chen,Z.
TITLE Human cytokine receptor
JOURNAL Patent: WO 0140467-A 14 07-JUN-2001;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1116
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CDS 21. .560
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BASE COUNT 336 a 229 c 222 g 329 t
ORIGIN

Query Match 100.0%; Score 1116; DB 6; Length 1116;
Best Local Similarity 100.0%; Pred. No. 1.7e-211;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1081 tgtttatttgacctcaataaacacttggatatccta 1116
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RESULT 2
AX179578
LOCUS AX179578 1116 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 1 from Patent WO0146422.
ACCESSION AX179578
VERSION AX179578.1 GI:15132010
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Presnell,S.R. and Kindsvogel,W.
TITLE Cytokine zcytol8
JOURNAL Patent: WO 0146422-A 1 28-JUN-2001;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
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BASE COUNT 336 a 229 c 222 g 329 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.7e-211;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Qy    901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Db    901 GCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGA 960

Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Qy   1081 tgtttatttgacctcaataaacacttggatatccta 1116
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Db   1081 TGTTTATTTGACCTCAATAAACACTTGGATATCCTA 1116


RESULT   3
AF279437
LOCUS       AF279437                1167 bp    mRNA    linear   PRI 09-OCT-2000
DEFINITION  Homo sapiens interleukin 22 (IL22) mRNA, complete cds.
ACCESSION   AF279437
VERSION     AF279437.1  GI:10719561
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1167)
  AUTHORS   Xie,M.H., Aggarwal,S., Ho,W.H., Foster,J., Zhang,Z., Stinson,J.,
            Wood,W.I., Goddard,A.D. and Gurney,A.L.
  TITLE     Interleukin (IL)-22, a Novel Human Cytokine That Signals through
            the Interferon Receptor-related Proteins CRF2-4 and IL-22R
  JOURNAL   J. Biol. Chem. 275 (40), 31335-31339 (2000)
   PUBMED   10875937
REFERENCE   2  (bases 1 to 1167)
  AUTHORS   Xie,M.-H., Aggarwal,S., Ho,W.-H., Foster,J., Zhang,Z., Stinson,J.,
            Wood,W.I., Goddard,A.D. and Gurney,A.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2000) Molecular Biology, Genentech Inc., 1 DNA
            Way, South San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .1167
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                     /chromosome="12"
                     /map="12q15"
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     CDS             58. .597
                     /gene="IL22"
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin 22"
                     /protein_id="AAG22064.1"
                     /db_xref="GI:10719562"
                     /translation="MAALQKSVSSFLMGTLATSCLLLLALLVQGGAAAPISSHCRLDK
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                     VLFPQSDRFQPYMQEVVPFLARLSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGE
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BASE COUNT      357 a    244 c    228 g    338 t
ORIGIN


  Query Match           99.9%;  Score 1114.4;  DB 9;  Length 1167;
  Best Local Similarity   99.9%;  Pred. No. 3.6e-211;
  Matches 1115;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
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Db     38 TCGAGTTAGAATTGTCTGCAATGGCCGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGG 97

Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     98 GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG 157

Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db    158 CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCA 217

Qy    181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Db    218 ACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTCGTC 277

Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Db    278 TCATTGGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGC 337

Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Db    338 AGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTT 397

Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Db    398 ATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATA 457

Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Db    458 TTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAA 517

Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Db    638 CTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAAGGAAGATGGG 697

Qy    661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
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Db    698 AAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGA 757

Qy    721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    758 AACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTTAT 817

Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 TGATAACATTTCATTGTAACTGGTGTTCTATACACAGAAAACAATTTATTTTTTAAATAA 877

Qy    841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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Qy    901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Db    938 GCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGA 997

Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Db   1058 TTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACA 1117

Qy   1081 tgtttatttgacctcaataaacacttggatatccta 1116
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Db   1118 TGTTTATTTGACCTCAATAAACACTTGGATATCCCA 1153


RESULT   4
AX092422
LOCUS       AX092422               1152 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 153 from Patent WO0116318.
ACCESSION   AX092422
VERSION     AX092422.1  GI:13444525
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1152)
  AUTHORS   Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
            Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0116318-A 153 08-MAR-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1152
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      342 a    244 c    228 g    338 t
ORIGIN


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  Matches 1114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
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Db     98 GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG 157

Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db    278 TCATTGGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGC 337

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Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
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Db    578 TGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTTCC 637

Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Qy    661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
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Db    698 AAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGA 757

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Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Db   1118 TGTTTATTTGACCTCAATAAACACTTGGATATCC 1151


RESULT   5
AX054620
LOCUS       AX054620               1139 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 1 from Patent WO0073457.
ACCESSION   AX054620
VERSION     AX054620.1  GI:12228184
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1139)
  AUTHORS   Parham,C.L., de waal Malefyt,R. and Marehalli,N.L.
  TITLE     Mammalian interleukin-10 homologs: il-d110 and il-d210
  JOURNAL   Patent: WO 0073457-A 1 07-DEC-2000;
            SCHERING CORPORATION (US)
FEATURES             Location/Qualifiers
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ORIGIN


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Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
           |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db     219 ACCGCACCTTCATGCTGGCTAAGGAGGNTAGCTTGGCTGATAACAACACAGACGTTCGTC 278

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     819 TGATAACATTTCATTGTAACTGGTGTTCTATACACAGAAAACAATTTATTTTTTAAATAA 878

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Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Db     999 CTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGATA 1058

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Db    1059 TTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACA 1118

Qy    1081 tgtttatttgacctcaataaa 1101
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Db    1119 TGTTTATNTGACCTCAATGAA 1139


RESULT   6
AX048204
LOCUS       AX048204               1132 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 44 from Patent WO0070049.
ACCESSION   AX048204
VERSION     AX048204.1  GI:11876994
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1132)
  AUTHORS   Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
            Azimzai,Y., Lu,D.A. and Patterson,C.
  TITLE     Extracellular signaling molecules
  JOURNAL   Patent: WO 0070049-A 44 23-NOV-2000;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1132
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 5571181CB1"
BASE COUNT      333 a    240 c    226 g    333 t
ORIGIN


  Query Match           97.7%;  Score 1090.4;  DB 6;  Length 1132;
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  Best Local Similarity   99.9%;  Pred. No. 2.1e-206;
  Matches 1091;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
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Db      31 TCGAGTTAGAATTGTCTGCAATGGCCGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGG 90

Qy      61 ggaccctggccaccagctgcctccttctctcttggccctcttggtacagggaggagcagctg 120
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Db      91 GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG 150

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db     151 CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCA 210

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Db     211 ACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTCGTC 270

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Db     271 TCATTGGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGC 330

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagccctt 360
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Db     331 AGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTT 390

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Db     391 ATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATA 450

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Db     511 AGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTC 570

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
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Db     571 TGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTTCC 630

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Db     631 CTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTTAACCAAAAGGAAGATGGG 690

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
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Db     691 AAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGA 750

Qy     721 aaccaatgccactttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
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Db     751 AACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTTAT 810

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Db     811 TGATAACATTTCATTGTAACTGGTGTTCTATACACAGAAAACAATTTATTTTTTAAATAA 870

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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Db     871 TTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCCCTAAATA 930

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Db     931 GCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGA 990

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Db     991 CTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGATA 1050

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Db    1051 TTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACA 1110

Qy    1081 tgtttatttgac 1092
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Db    1111 TGTTTATTTGCC 1122


RESULT   7
HSA277247
LOCUS       HSA277247                690 bp    mRNA    linear   PRI 21-DEC-2000
DEFINITION  Homo sapiens mRNA for interleukin 22 (IL-22 gene).
ACCESSION   AJ277247
VERSION     AJ277247.1  GI:9968293
KEYWORDS    IL-22 gene; interleukin 22.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Dumoutier,L., Van Roost,E., Colau,D. and Renauld,J.C.
  TITLE     Human interleukin-10-related T cell-derived inducible factor:
            molecular cloning and functional characterization as an
            hepatocyte-stimulating factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (18), 10144-10149 (2000)
  MEDLINE   20420346
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Renauld,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) Renauld J.C., UCL 74.59, Ludwig Institute
            for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
            BELGIUM
FEATURES             Location/Qualifiers
     source          1. .690
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                     /db_xref="taxon:9606"
                     /cell_type="peripheral blood mononuclear cells"
     gene            72. .611
                     /gene="IL-22"
     CDS             72. .611
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                     /codon_start=1
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                     /db_xref="GI:9968294"
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                     SNFQQPYITNRTFMLAKEASLADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLEE
                     VLFPQSDRFQPYMQEVVPFLARLSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGE
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BASE COUNT      182 a    176 c    167 g    165 t
ORIGIN


  Query Match           57.3%;  Score 639;  DB 9;  Length 690;
  Best Local Similarity  100.0%;  Pred. No. 7.2e-117;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
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Db      52 TCGAGTTAGAATTGTCTGCAATGGCCGCCCTGCAGAAATCTGTGAGCTCTTTCCTTATGG 111

Qy      61 ggaccctggccaccagctgcctccttctctcttggccctcttggtacagggaggagcagctg 120
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Db     112 GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db     172 CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCA 231

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Db     232 ACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTCGTC 291
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Db    292 TCATTGGGGAGAAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCTATCTGATGAAGC 351

Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Db    352 AGGTGCTGAACTTCACCCTTGAAGAAGTGCTGTTCCCTCAATCTGATAGGTTCCAGCCTT 411

Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Db    412 ATATGCAGGAGGTGGTGCCCTTCCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCATA 471

Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Db    472 TTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAA 531

Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Db    532 AGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTC 591

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
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Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttt 639
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Db    652 CTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTT 690


RESULT   8
AF387519
LOCUS       AF387519               8393 bp    DNA     linear   PRI 14-JUN-2001
DEFINITION  Homo sapiens interleukin 22 (IL22) gene, complete cds.
ACCESSION   AF387519
VERSION     AF387519.1  GI:14423570
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8393)
  AUTHORS   Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
            Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-2001) Molecular Biotechnology, University of
            Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI Program for
            Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.mbt.washington.edu).
FEATURES             Location/Qualifiers
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                     6685. .6841)
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     gene            2056. .6841
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                /rpt_type=dispersed
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     variation  5553
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  Query Match          57.0%;  Score 636.4;  DB 9;  Length 8393;
  Best Local Similarity  99.8%;  Pred. No. 2.5e-116;
  Matches  637;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
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Db    6681 ACAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTC 6740

Qy     539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttt 598
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Db    6741 TCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTT 6800

Qy     599 ccctgctagaaataacaattagatgccccaaagcgatttttttaaccaaaaggaagatg 658
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Db    6801 CCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAAGGAAGATG 6860

Qy     659 ggaagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaag 718
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Db    6861 GGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAG 6920

Qy     719 gaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatattt 778
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Db    6921 GAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTT 6980

Qy     779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaat 838
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Db    6981 ATTGATAACATTTCATTGTAACTGGTGTTCTATACACAGAAAACAATTTATTTTTAAAT 7040

Qy     839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaa 898
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Db    7041 AATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCCCTAAA 7100

Qy     899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
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Db    7101 TAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAA 7160

Qy     959 gactgcattttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
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Db    7161 GACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGA 7220

Qy    1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
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Db    7221 TATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAA 7280

Qy    1079 catgtttatttgacctcaataaacacttggatatccta 1116
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Db    7281 CATGTTTATTTGACCTCAATAAACACTTGGATATCCTA 7318


RESULT   9
AC022511/c
LOCUS       AC022511               133350 bp    DNA     linear   PRI 11-JUL-2001
DEFINITION  Homo sapiens 12 BAC RP11-71J4 (Roswell Park Cancer Institute Human
            BAC Library) complete sequence.
ACCESSION   AC022511
VERSION     AC022511.22  GI:14669924
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 133350)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 133350)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 133350)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Jul 11, 2001 this sequence version replaced gi:12656660.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT----------

---------- Summary Statistics ----------

Contig length:	150667
Phrap values in estimate:	149705
Average error rate (BCM-Phrap estimate):	1.52849e-05
Fraction of Phrap values less than 40 :	0.0163588
Number of consensus changing edits:	83
Number of N's in consensus :	0

---------- Consensus changing edits ----------

Position	Original+Context	Edited+Context
7824	tattatatat(n)nnngtatact	tattatatat(g)tgtgtatact
7825	attatatatn(n)nngtatacta	attatatatg(t)gtgtatacta
7826	ttatatatnn(n)ngtatactat	ttatatatgt(g)tgtatactat
7827	tatatatnnn(n)gtatactata	tatatatgtg(t)gtatactata
7855	atatatatgc(n)acattttata	atatatatgc(a)acattttata
8162	agaccacttt(n)tgagatggca	agaccacttt(t)tgagatggca
10049	tgggcagatc(n)cnnnnngnnn	tgggcagatc(a)cctgaggtca
10051	ggcagatcnc(n)nnnngnnnnn	ggcagatcac(c)tgaggtcagg
10052	gcagatcncn(n)nnngnnnnnn	gcagatcacc(t)gaggtcagga
10053	cagatcncnn(n)nngnnnnnng	cagatcacct(g)aggtcaggag
10054	agatcncnnn(n)ngnnnnnngn	agatcacctg(a)ggtcaggagt
10055	gatcncnnnn(n)gnnnnnngnn	gatcacctga(g)gtcaggagtt
10057	tcncnnnnng(n)nnnngnntn	tcacctgagg(t)caggagtttg
10058	cncnnnnngn(n)nnngnntnn	cacctgaggt(c)aggagtttga
10059	ncnnnnngnn(n)nngnntnng	acctgaggtc(a)ggagtttgag
10060	cnnnngnnn(n)nngnntnnga	cctgaggtca(g)gagtttgaga
10061	nnnngnnnn(n)ngnntnngac	ctgaggtcag(g)agtttgagac
10062	nnngnnnnn(n)gnntnngact	tgaggtcagg(a)gtttgagact
10064	nngnnnnnng(n)ntnngactag	aggtcaggag(t)ttgagactag
10065	ngnnnnnngn(n)tnngactagt	ggtcaggagt(t)tgagactagt
10067	nnnnngnnt(n)ngactagtct	tcaggagttt(g)agactagtct
10068	nnnngnntn(n)gactagtctg	caggagtttg(a)gactagtctg
10094	catggtgaaa(n)cctgtctnta	catggtgaaa(c)cctgtctcta
10102	aancctgtct(n)tactaaaaan	aaccctgtct(c)tactaaaaat
10112	ntactaaaaa(n)acaaaaatta	ctactaaaaa(t)acaaaaatta
10287	atggaagaga(n)tgtgggtata	atggaagaga(t)tgtgggtata
19854	aaatctgaat(n)aaaangccca	aaatctgaat(t)aaaatgccca
19859	tgaatnaaaa(n)gcccaggtta	tgaattaaaa(t)gcccaggtta
19882	tttctatctc(n)ctgactnaan	tttctatctc(c)ctgactagat
19889	ctcnctgact(n)aannnnnnnt	ctccctgact(a)gatggccagt
19890	tcnctgactn(a)annnnnnntn	tccctgacta(g)atggccagtt
19892	nctgactnaa(n)nnnnnntnnn	cctgactaga(t)ggccagttcc
19893	ctgactnaan(n)nnnnntnnnn	ctgactagat(g)gccagttcca
19894	tgactnaann(n)nnnntnnnnc	tgactagatg(g)ccagttccat
19895	gactnaannn(n)nnntnnnncn	gactagatgg(c)cagttccatt
19896	actnaannnn(n)nntnnnncnn	actagatggc(c)agttccatta

```
19897    ctnaannnnn(n)ntnnnncnnn    ctagatggcc(a)gttccattag
19898    tnaannnnnn(n)tnnnncnnnt    tagatggcca(g)ttccattagg
19900    aannnnnnnt(n)nnncnnnttn    gatggccagt(t)ccattagggc
19901    annnnnnntn(n)nncnnnttnn    atggccagtt(c)cattagggca
19902    nnnnnnntnn(n)ncnnnttnng    tggccagttc(c)attagggcag
19903    nnnnnntnnn(n)cnnnttnngg    ggccagttcc(a)ttagggcagg
19904    nnnnntnnnn(c)nnnttnnggn    gccagttcca(t)tagggcagga
19905    nnnntnnnnc(n)nnttnnggna    ccagttccat(t)agggcaggaa
19906    nnntnnnncn(n)nttnnggnaa    cagttccatt(a)gggcaggaaa
19907    nntnnnncnn(n)ttnnggnaac    agttccatta(g)ggcaggaaac
19908    ntnnnncnnn(t)tnnggnaaca    gttccattag(g)gcaggaaaca
19909    tnnnncnnnt(t)nnggnaacan    ttccattagg(g)caggaaacaa
19910    nnnncnnntt(n)nggnaacanc    tccattaggg(c)aggaaacaag
19911    nnncnnnttn(n)ggnaacanca    ccattagggc(a)ggaaacaaga
19914    cnnnttnngg(n)aacancacag    ttagggcagg(a)aacaagacag
19919    tnnggnaaca(n)cacaggtcan    gcaggaaaca(a)gacaggtcag
19920    nnggnaacan(c)acaggtcana    caggaaacaa(g)acaggtcaga
19929    ncacaggtca(n)atttttctgg    agacaggtca(g)atttttctgg
19959    gtaattccag(n)aaanaccacn    gtaattccag(t)aaatacccact
19963    ttccagnaaa(n)accacngttn    ttccagtaaa(t)accactgttt
19969    naaanaccac(n)gttnctctct    taaataccac(t)gtttctctct
19973    naccacngtt(n)ctctctctct    taccactgtt(t)ctctctctct
43356    actatcattg(n)agttatgagt    actatcattg(a)agttatgagt
61290    aagaccctgt(n)tcaaaaaaaa    aagaccctgt(c)tcaaaaaaaa
92985    tatattatct(n)aaatttaact    tatattatct(g)aaatttaact
93027    cagacatatg(a)gtgcatnctt    cagacatatg(t)gtgcatgctt
93034    atgagtgcat(n)cttgatntcc    atgtgtgcat(g)cttgatgtcc
93041    catncttgat(n)tccctattaa    catgcttgat(g)tccctcttaa
93047    tgatntccct(a)ttaaaactct    tgatgtccct(c)ttaaaactct
93107    attcatctca(n)tttcctctta    attcatctca(a)tttcctctta
105875   aaatgccatg(n)caatgtcagg    aaatgccatg(g)caatgtcagg
124584   aagtccatgt(n)ngtaggaact    aagtccatgt(a)cgtaggaact
124585   agtccatgtn(n)gtaggaacta    agtccatgta(c)gtaggaacta
125786   ctggccaaca(n)ggtgaaaccc    ctggccaaca(t)ggtgaaaccc
125860   tcccagctac(n)nnnnaggctg    tcccagctac(t)cgggaggctg
125861   cccagctacn(n)nnnaggctga    cccagctact(c)gggaggctga
125862   ccagctacnn(n)nnaggctgag    ccagctactc(g)ggaggctgag
125863   cagctacnnn(n)naggctgagg    cagctactcg(g)gaggctgagg
125864   agctacnnnn(n)aggctgaggc    agctactcgg(g)aggctgaggc
126773   ttttcttttg(c)tttttttctt    ttttcttttg(t)tttttttctt
126811   acggagtctc(n)ntctatnnnc    acggagtctc(g)ctctatcgcc
126812   cggagtctcn(n)tctatnnncc    cggagtctcg(c)tctatcgccc
126818   ctcnntctat(n)nnccnggctg    ctcgctctat(c)gcccaggctg
126819   tcnntctatn(n)nccnggctgg    tcgctctatc(g)cccaggctgg
126820   cnntctatnn(n)ccnggctgga    cgctctatcg(c)ccaggctgga
126823   tctatnnncc(n)ggctggagtg    tctatcgccc(a)ggctggagtg
```

Query Match 57.0%; Score 636.4; DB 9; Length 133350;
Best Local Similarity 99.8%; Pred. No. 2.6e-116;
Matches 637; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy    479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
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Db   2235 ACAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTC 2176

Qy    539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttt 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2175 TCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTT 2116

Qy    599 ccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatg 658
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Qy    719 gaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatattt 778
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Db   1995 GAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTT 1936

Qy    779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaat 838
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Qy    839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaa 898
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Qy    899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
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Qy    959 gactgcattttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
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Db   1755 GACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGA 1696

Qy   1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
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Db   1695 TATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAA 1636

Qy   1079 catgtttatttgacctcaataaacacttggatatccta 1116
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Db   1635 CATGTTTATTTGACCTCAATAAACACTTGGATATCCTA 1598
```

RESULT 10
AC007458/c
LOCUS AC007458 191111 bp DNA linear PRI 25-MAR-2000
DEFINITION Homo sapiens 12q15 BAC RPCI11-444B24 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
ACCESSION AC007458
VERSION AC007458.13 GI:5668755
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 191111)
AUTHORS Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H., Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S., Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W., Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A., Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L., Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M., Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati,R., Nelson,D., Nickerson,E. and Gibbs,R.A.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 191111)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 191111)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 191111)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 5 (bases 1 to 191111)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 6 (bases 1 to 191111)
AUTHORS Worley,K.C.
TITLE Direct Submission

JOURNAL Submitted (25-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Jul 31, 1999 this sequence version replaced gi:5230396.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT----------

--------------- Summary Statistics ---------------

Contig length:	151624
Phrap values in estimate:	151315
Average error rate (BCM-Phrap estimate):	0.000165522
Fraction of Phrap values less than 40 :	0.020725
Number of consensus changing edits:	5
Number of N's in consensus :	0

--------------- Consensus changing edits ---------------

Position	Original+Context	Edited+Context
2273	ggccttcatt(n)tcaattgttt	ggccttcatt(t)tcaattgttt
5088	agatgggtgc(n)tactccttcc	agatgggtgc(c)tactccttcc
102880	ggtttcactg(n)gttaatcagg	ggtttcactg(t)gttaatcagg
123710	tcttataatt(n)tgtttatatg	tcttataatt(t)tgtttatatg
127972	ttttcttgag(n)gaatcctaag	ttttcttgag(t)gaatcctaag

--------- Distribution of Quality < 40 Bases ----------

Version: 1.01 qxfo.

FEATURES	Location/Qualifiers
source	1. .191111
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	/db_xref="taxon:9606"
	/chromosome="12q15"
	/clone="RPCI11-444B24"
repeat_region	complement(1. .3489)
	/rpt_family="L1P3"
misc_feature	1. .82
	/note="Overlaps bases 113681. .113762 in clone AC005294"
	/function="Overlaps with adjacent clone AC005294"
repeat_region	complement(3702. .4041)
	/rpt_family="L1P3"
repeat_region	complement(4043. .7146)
	/rpt_family="L1PBb"
repeat_region	complement(7625. .7930)
	/rpt_family="L1PA15-16"
repeat_region	complement(8427. .8844)
	/rpt_family="L1M2"
repeat_region	complement(8860. .8988)
	/rpt_family="MLT1D"
repeat_region	complement(8997. .9284)
	/rpt_family="L1MC/D"
repeat_region	complement(9927. .10097)
	/rpt_family="L1M4"
repeat_region	10575. .10852
	/rpt_family="AluJo"
repeat_region	11022. .11060
	/rpt_family="AT_rich"
repeat_region	complement(12158. .12355)
	/rpt_family="MER20"
repeat_region	complement(12407. .12592)
	/rpt_family="MIR"
repeat_region	12877. .12950
	/rpt_family="AT_rich"
repeat_region	14057. .14169
	/rpt_family="MIR"
repeat_region	14920. .14949
	/rpt_family="(TG)n"
repeat_region	complement(15199. .15978)
	/rpt_family="L1MA9"
repeat_region	16201. .16508
	/rpt_family="AluSx"
repeat_region	16931. .17096
	/rpt_family="MIR"
repeat_region	complement(17098. .17247)
	/rpt_family="MIR"
repeat_region	17645. .17841
	/rpt_family="MER107"
repeat_region	complement(18996. .19099)
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repeat_region	complement(21141. .21217)
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repeat_region	21218. .21247
	/rpt_family="(CA)n"
repeat_region	complement(21248. .21454)
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	/rpt_family="LTR9B"
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	/rpt_family="THE1B"
repeat_region	complement(22381. .23987)

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                     /rpt_family="L2"
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  Query Match             57.0%;  Score 636.4;  DB 9;  Length 191111;
  Best Local Similarity   99.8%;  Pred. No. 2.6e-116;
  Matches  637;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
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Db 188245 ACAGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTC 188186

Qy     539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttt 598
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 188185 TCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTT 188126

Qy     599 ccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatg 658
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Db 188125 CCCTGCTAGAAATAACAATTAGATGCCCCAAAGCGATTTTTTTTTAACCAAAAGGAAGATG 188066

Qy     659 ggaagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaag 718
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 188065 GGAAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAG 188006

Qy     719 gaaaccaatgccactttgtttataagaccagaaggtagactttctaagcatagatatttt 778
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Db 188005 GAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTT 187946

Qy     779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaat 838
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Db 187945 ATTGATAACATTTCATTGTAACTGGTGTTCTATACACAGAAAACAATTTATTTTTTAAAT 187886

Qy     839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaa 898
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Db 187885 AATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAAAAAACCCCTAAA 187826

Qy     899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
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Db 187825 TAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAA 187766

Qy     959 gactgcatttttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
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Db 187765 GACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGA 187706

Qy    1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
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Db 187705 TATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAA 187646

Qy    1079 catgtttatttgacctcaataaacacttggatatccta 1116
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Db 187645 CATGTTTATTTGACCTCAATAAACACTTGGATATCCTA 187608


RESULT  11
AC087562
LOCUS       AC087562               135146 bp    DNA     linear   HTG 19-OCT-2001
DEFINITION  Pan troglodytes clone RP43-74I17, WORKING DRAFT SEQUENCE, 31
            unordered pieces.
ACCESSION   AC087562
VERSION     AC087562.4  GI:14190648
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 135146)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
            Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
            Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
            Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
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            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
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            Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
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            Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
            Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
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            Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
            Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
            Morgan,M., Morris,S., Moser,M., Neal,D., Newtson,J., Newtson,N.,
            Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S.,
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            Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M.,
            Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N.,
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            Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
            Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
            Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
    TITLE   Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 135146)
  AUTHORS   Worley,K.C.
    TITLE   Direct Submission
  JOURNAL   Submitted (10-JAN-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 23, 2001 this sequence version replaced gi:12621390.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: ZUAE
                Center clone name: RP43-74I17
            -------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-primer Bodipy: 49% of reads
                Chemistry: Dye-terminator Big Dye: 51% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 134068 bases at least Q40
                Consensus quality: 143074 bases at least Q30
                Consensus quality: 148054 bases at least Q20
                Estimated insert size: 144346; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 31 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
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          * be preserved.
          *        1    10537: contig of 10537 bp in length
          *    10538    10637: gap of unknown length
          *    10638    16496: contig of 5859 bp in length
          *    16497    16596: gap of unknown length
          *    16597    22635: contig of 6039 bp in length
          *    22636    22735: gap of unknown length
          *    22736    28745: contig of 6010 bp in length
          *    28746    28845: gap of unknown length
          *    28846    34084: contig of 5239 bp in length
          *    34085    34184: gap of unknown length
          *    34185    39046: contig of 4862 bp in length
          *    39047    39146: gap of unknown length
          *    39147    44980: contig of 5834 bp in length
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          *    45081    48686: contig of 3606 bp in length
          *    48687    48786: gap of unknown length
          *    48787    54719: contig of 5933 bp in length
          *    54720    54819: gap of unknown length
          *    54820    59584: contig of 4765 bp in length
          *    59585    59684: gap of unknown length
          *    59685    65244: contig of 5560 bp in length
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          *    65345    70092: contig of 4748 bp in length
          *    70093    70192: gap of unknown length
          *    70193    75303: contig of 5111 bp in length
          *    75304    75403: gap of unknown length
          *    75404    79784: contig of 4381 bp in length
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          *    88750    92541: contig of 3792 bp in length
          *    92542    92641: gap of unknown length
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          *   100993   103932: contig of 2940 bp in length
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          *   104033   107186: contig of 3154 bp in length
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          *   110320   113001: contig of 2682 bp in length
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          *   113102   115998: contig of 2897 bp in length
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          *   119434   122281: contig of 2848 bp in length
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          *   122382   125109: contig of 2728 bp in length
          *   125110   125209: gap of unknown length
          *   125210   127912: contig of 2703 bp in length
          *   127913   128012: gap of unknown length
          *   128013   130629: contig of 2617 bp in length
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                     /db_xref="taxon:9598"
                     /clone="RP43-74I17"
BASE COUNT    40919 a  26449 c  25229 g  39519 t   3030 others
ORIGIN


  Query Match           50.5%;  Score 564;  DB 2;  Length 135146;
  Best Local Similarity   98.0%;  Pred. No. 6.1e-102;
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Db   28847 GAGAACTGGATTTGCTGTATATGTCTCTGAGAAATGCCTGCATTTGACCAGAGCAAAGCG 28906

Qy     574 gaaaaatgaataactaacccccttttccctgctagaaataacaattagatgccccaaagcg 633
           |||| ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   28907 GAAAGATGAATAACTAACCCCCTTTTCCTGCTAGAAATAACAATTAGATGCCCCAAAGCG 28966

Qy     634 a-ttttttttaaccaaaaggaagatgggaagccaaactccatcatgatgggtggattcca 692
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Db   28967 ACTTTTTTTTAACCAAAAGGAAGATGGGAAGCCAAACTCCATCATGATTGGTGGATTCCA 29026

Qy     693 aatgaacccctgcgttagttacaaaggaaaccaatgccacttttgtttataagaccagaa 752
           |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db   29027 AATGAACCCCTGTTTTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAA 29086

Qy     753 ggtagactttctaagcatagatatttattgataacatttcattgtaactggtgttctata 812
           |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29087 GGTAGACTTTTTAAGCATAGATATTTATTGATAACATTTCATTGTAACTGGTGTTCTATA 29146

Qy     813 cacagaaaacaatttatttttaaataattgtctttttccataaaaaagattactttcca 872
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29147 CACAGAAAACAATTTATTTTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCA 29206

Qy     873 ttcctttaggggaaaaaacccctaaatagcttcatgtttccataatcagtactttatatt 932
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Db   29207 TTCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATT 29266

Qy     933 tataaatgtatttattattattataagactgcattttatttatatcattttattaatatg 992
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Db   29267 TATAAATGTATTTATTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATG 29326

Qy     993 gatttatttatagaaacatcattcgatattgctacttgagtgtaaggctaatattgatat 1052
           |||||||||||||||| ||||||||||||||||||||||||| ||||||||||||||||||
Db   29327 GATTTATTTATAGAAGCATCATTCGATATTGCTACTTGAGTATAAGGCTAATATTGATAT 29386

Qy    1053 ttatgacaataattatagagctataacatgtttatttgacctcaataaacacttggatat 1112
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Db   29387 TTATGACAATAATTATAG-GCTATAACATGTTTATTTGACCTCAATAAACACTTGGATAT 29445

Qy    1113 ccta 1116
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Db   29446 CCTA 29449


RESULT  12
AR165228
LOCUS       AR165228                1111 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 9 from patent US 6274710.
ACCESSION   AR165228
VERSION     AR165228.1  GI:16238721
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1111)
  AUTHORS   Dumoutier,L., Louhed,J. and Renauld,J.
  TITLE     Antibodies which specifically bind T Cell inducible factors (TIFs)
  JOURNAL   Patent: US 6274710-A 9 14-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .1111
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BASE COUNT      346 a    232 c    236 g    297 t
ORIGIN


  Query Match           47.1%;  Score 525.2;  DB 6;  Length 1111;
  Best Local Similarity   73.8%;  Pred. No. 2.7e-94;
  Matches  813;  Conservative    0;  Mismatches  253;  Indels   36;  Gaps   10;

Qy      15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74
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Db     44 TCGGTGATGGCTGTCCTGCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGCCGCC 103

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Db    104 AGCTGCCTGCTTCTCATTGCCCTGTGGGCCCAGGAGGCAAATGCGCTGCCCATCAACACC 163

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
Db    164 CGGTGCAAGCTTGAGGTGTCCAACTTCCAGCAGCCGTACATCGTCAACCGCACCTTTATG 223

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
Db    224 CTGGCCAAGGAGGCCAGCCTTGCAGATAACAACACAGACGTCCGGCTCATCGGGGAGAAA 283

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
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Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
Db    344 ACCCTGGAAGACATTCTGCTCCCCCAGTCAGACAGGTTCCGGCCCTACATGCAGGAGGTG 403

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
Db    404 GTGCCTTTCCTGACCAAACTCAGCAATCAGCTCAGCTCCTGTCACATCAGTGGTGACGAC 463

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
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Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
Db    524 GGAGAGATCAAAGCGATCGGGGAACTGGACCTGCTGTTTATGTCTCTGAGAAATGCTTGC 583

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttccctgctagaaataac 614
Db    584 GTCTGAGCGAGAAGAAGCTAGAAAACGAAGAACTGCTCCTTCCTGCCTTCTAAAAAGAAC 643

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
Db    644 AATAAGATCCCTGAATGGACTTTTTTA----CTAAAGGAAAGTGAGAAGCTAACGTCCAC 699

Qy    675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccactt 734
Db    700 CATCATTAGAAGATTTCACATGAAACCTGGCTCAGTTGAAAGAGAAAATAGTGTCAA--G 757

Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
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Db    866 AAAGGAGGTTACCTCTCATTCCTCTA---GAAGAAAAGCCTATGTAACTTCA--TTTCCA 920

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
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Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
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Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
Db   1035 TAAAGCAAATA---ATATTTATGATAATAACTATAG----AAACAAGATATCTTAGGCTT 1087

Qy   1095 caataaacacttggatatccta 1116
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Db   1088 TAATAAACACATGAATATCATA 1109


RESULT 13
MMU249492
LOCUS       MMU249492              1118 bp    mRNA    linear   ROD 16-FEB-2000
DEFINITION  Mus musculus mRNA for TIF beta protein (IL-TIFb gene).
ACCESSION   AJ249492
VERSION     AJ249492.1  GI:6996555
KEYWORDS    IL-TIFb gene; TIF beta protein.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1118)
  AUTHORS   Dumoutier,L., Louahed,J. and Renauld,J.C.
  TITLE     Cloning and characterization of TIF, a new IL-10-related cytokine
            induced by IL-9
  JOURNAL   Immunology 164, 1814-1819 (2000)
REFERENCE   2  (bases 1 to 1118)
  AUTHORS   Renauld,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1999) Renauld J.C., Cytokine group, Ludwig
            Institute for Cancer Research, 74, Avenue Hippocrate, Brussels,
            B-1200, BELGIUM
FEATURES             Location/Qualifiers
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                     /strain="129"
                     /db_xref="taxon:10090"
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                     /gene="IL-TIFb"
     CDS             50. .589
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                     /function="cytokine"
                     /codon_start=1
                     /product="TIF beta protein"
                     /protein_id="CAB75547.1"
                     /db_xref="GI:6996556"
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BASE COUNT      353 a    233 c    235 g    297 t
ORIGIN


  Query Match           47.1%;  Score 525.2;  DB 10;  Length 1118;
  Best Local Similarity   73.8%;  Pred. No. 2.7e-94;
  Matches  813;  Conservative    0;  Mismatches  253;  Indels   36;  Gaps   10;

Qy     15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74
Db     44 TCGGTGATGGCTGTCCTGCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGCCGCC 103

Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
Db    104 AGCTGCCTGCTTCTCATTGCCCTGTGGGCCCAGGAGGCAAATGCGCTGCCCATCAACACC 163

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
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Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
Db    224 CTGGCCAAGGAGGCCAGCCTTGCAGATAACAACACAGACGTCCGGCTCATCGGGGAGAAA 283

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
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Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
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Db    344 ACCCTGGAAGACATTCTGCTCCCCCAGTCAGACAGGTTCCGGCCCTACATGCAGGAGGTG 403

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
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Db    404 GTGCCTTTCCTGACCAAACTCAGCAATCAGCTCAGCTCCTGTCACATCAGTGGTGACGAC 463

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
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Db    464 CAGAACATCCAGAAGAATGTCAGAAGGCTGAAGGAGACAGTGAAAAAGCTTGGAGAGAGC 523

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
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Db    524 GGAGAGATCAAAGCGATCGGGGAACTGGACCTGCTGTTTATGTCTCTGAGAAATGCTTGC 583

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttttccctgctagaaataac 614
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Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
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Db    758 TTGTCCATGAGACCAG-AGGTAGACTTGATAACCACAAAGATTCATTGACAATATTTTAT 816

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Db    817 TGTCATTGAT----AATGCAACAGAAAAAGTATGTACTTTAAAAAATTGTTT-------G 865

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttcca 914
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Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
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Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
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RESULT  14
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LOCUS       AR165226               1119 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 7 from patent US 6274710.
ACCESSION   AR165226
VERSION     AR165226.1  GI:16238719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1119)
  AUTHORS   Dumoutier,L., Louhed,J. and Renauld,J.
  TITLE     Antibodies which specifically bind T Cell inducible factors (TIFs)
  JOURNAL   Patent: US 6274710-A 7 14-AUG-2001;
FEATURES             Location/Qualifiers
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BASE COUNT      352 a    233 c    232 g    302 t
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  Query Match           47.0%;  Score 524.4;  DB 6;  Length 1119;
  Best Local Similarity  74.3%;  Pred. No. 3.9e-94;
  Matches  819;  Conservative    0;  Mismatches  246;  Indels   37;  Gaps   11;

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Qy     495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
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Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
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Db   1089 TAATAAACACATGGATATCATA 1110


RESULT  15
MMU249491
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DEFINITION  Mus musculus mRNA for TIF alpha protein (IL-22 gene).
ACCESSION   AJ249491
VERSION     AJ249491.1  GI:6996553
KEYWORDS    IL-2 gene; IL-TIFa gene; TIF alpha protein.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1121)
  AUTHORS   Dumoutier,L., Louahed,J. and Renauld,J.C.
  TITLE     Cloning and characterization of IL-10-related T Cell-derived
            inducible factor (IL-TIF), a novel cytokine structurally related to
            IL-10 and inducible by IL-9
  JOURNAL   Immunology 164, 1814-1819 (2000)
REFERENCE   2  (bases 1 to 1121)
  AUTHORS   Renauld,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1999) Renauld J.C., Cytokine group, Ludwig
            Institute for Cancer Research, 74, Avenue Hippocrate, Brussels,
            B-1200, BELGIUM
FEATURES             Location/Qualifiers
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BASE COUNT      352 a    235 c    232 g    302 t
ORIGIN


  Query Match           47.0%;  Score 524.4;  DB 10;  Length 1121;
  Best Local Similarity  74.3%;  Pred. No. 3.9e-94;
  Matches  819;  Conservative    0;  Mismatches  246;  Indels   37;  Gaps   11;

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Db      48 TCTCTGATGGCTGTCCTGCAGAAATCTATGAGTTTTTCCCTTATGGGGACTTTGGCCGCC 107

Qy      75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
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Qy     135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
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Qy     255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
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Qy     315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
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Qy     435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
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Qy     675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccactt 734
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Qy     735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
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Qy     915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
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Qy     975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:32:14 ; Search time 217.44 Seconds
(without alignments)
8811.978 Million cell updates/sec

Title: US-09-746-375-1
Perfect score: 1116
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttggatatccta 1116

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	1116	100.0	1116	22	AAD09719	Human cytokine, ZC
	2	1116	100.0	1116	22	AAF83741	Human IL-TIF polyp
	3	1116	100.0	1177	21	AAC81773	Human GIL-19/AE289
	4	1114	99.8	1152	22	AAF92134	Human PRO10096 cDN
	5	1114	99.8	1152	22	AAC87053	Nucleotide sequenc
	6	1096.6	98.3	1139	22	AAF28841	Human interleukin-
	7	1090.4	97.7	1132	22	AAC84310	Human EXCS encodin
	8	639	57.3	690	21	AAA28839	Human T cell induc
	9	639	57.3	690	22	AAS14875	Human cDNA encodin
	10	526	47.1	1166	21	AAC81774	Murine GIL-19 prot
	11	525.2	47.1	1111	21	AAA28817	Murine T cell indu
	12	525.2	47.1	1111	22	AAS14860	Mouse cDNA for T c
	13	524.4	47.0	1119	21	AAA28815	Murine T cell indu
	14	524.4	47.0	1119	22	AAS14858	Mouse cDNA encodin
	15	429.2	38.5	778	22	AAD09746	Mouse ZCYTO18 cDNA
	16	380	34.1	537	22	AAF28842	Human interleukin-
	17	356.4	31.9	501	22	AAD09720	Degenerate sequenc
	18	270.4	24.2	504	21	AAA43454	Mouse secreted exp
	19	216.4	19.4	5935	21	AAA28818	Murine T cell indu
	20	216.4	19.4	5935	22	AAS14878	Mouse partial geno
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	22	215.6	19.3	7445	22	AAS14859	Mouse partial geno
	23	207	18.5	4796	21	AAA28840	Human T cell induc
	24	207	18.5	4797	22	AAS14876	Human partial geno
c	25	67.4	6.0	3296	23	ABL17264	Drosophila melanog
c	26	63.2	5.7	6243	20	AAZ09598	Clostridium specie
	27	62	5.6	6082	24	ABL33752	Human immune syste
c	28	61	5.5	113515	24	ABL34175	Human immune syste
	29	60.4	5.4	14987	24	ABL32630	Human immune syste
	30	60.2	5.4	7597	24	ABL33013	Human immune syste
c	31	59.8	5.4	19965	22	AAK73166	Human immune/haema
	32	59.6	5.3	5413	22	AAS46694	Tumour suppressor
c	33	59.6	5.3	20420	22	AAK73165	Human immune/haema
	34	59.4	5.3	5975	24	AAS61096	Human gene regulat
c	35	59.2	5.3	8786	23	ABL16590	Drosophila melanog
c	36	58.8	5.3	740	22	AAS42953	DNA encoding G pro
c	37	58.2	5.2	5487	24	ABL33598	Human immune syste
c	38	58.2	5.2	7456	24	ABL33931	Human immune syste
c	39	58	5.2	6641	24	ABL32315	Human immune syste
	40	57.6	5.2	20420	22	AAK73165	Human immune/haema
	41	57	5.1	6971	24	ABL33237	Human immune syste
c	42	56.8	5.1	19124	18	AAT72882	Plasmodium var-7 g
c	43	56.8	5.1	19124	21	AAZ98287	Plasmodium var-7 p
	44	56.6	5.1	6175	24	ABL33307	Human immune syste
c	45	56.6	5.1	6298	22	AAS45359	Chemically pretrea

ALIGNMENTS

RESULT 1
AAD09719
ID AAD09719 standard; cDNA; 1116 BP.
XX
AC AAD09719;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human cytokine, ZCYTO18 cDNA.
XX
KW Human; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW cancer; inflammation; gene therapy; chromosome 12; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 21..560
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FT sig_peptide 57..119
FT /*tag= e
FT mat_peptide 120..557
FT /*tag= f
FT /product= "Human mature ZCYTO18 protein #2"

XX
PN WO200146422-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000WO-US35308.
XX
PR 23-DEC-1999; 99US-0471767.
PR 01-DEC-2000; 2000US-0250841.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Kindsvogel W;
XX
DR WPI; 2001-408648/43.
DR P-PSDB; AAE04538, AAE04539.
XX
PT Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS Claim 2; Page 140-142; 167pp; English.
XX
CC The patent discloses novel human cytokine, ZCYTO18 protein and its
CC corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC killing cancer cells. It is useful for increasing platelets in a
CC patient or injured tissue. It is also used in gene therapy.
CC The present sequence is a cDNA encoding novel human cytokine, ZCYTO18
CC protein. ZCYTO18 DNA is located at the 12q15 region of chromosome 12.
XX
SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 100.0%; Score 1116; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.9e-233;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
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Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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RESULT 2
AAF83741
ID AAF83741 standard; cDNA; 1116 BP.
XX
AC AAF83741;
XX
DT 23-JUL-2001 (first entry)
XX
DE Human IL-TIF polypeptide encoding cDNA.
XX
KW Cytokine receptor; zcytor16; IL-TIF; antiinflammatory; cytostatic;
KW antirheumatic; antiarthritic; antiasthmatic; antiatherosclerotic;
KW immunosuppressive; chromosome 6q24.1-25.2; human; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 21..560
FT /*tag= a
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XX
PN WO200140467-A1.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US32703.
XX
PR 03-DEC-1999; 99US-0169049.
PR 13-SEP-2000; 2000US-0232219.
PR 31-OCT-2000; 2000US-0244610.

XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Kindsvogel W, Chen Z;
XX
DR WPI; 2001-356158/37.
DR P-PSDB; AAB62664.
XX
PT New soluble cytokine receptor polypeptides and polynucleotides, useful
PT for diagnosing and treating cancer and inflammatory conditions -
XX
PS Example 17; Page 193-195; 210pp; English.
XX
CC The invention relates to a human cytokine receptor polypeptide,
CC designated zcytor16. The zcytor16 polypeptide can be expressed by
CC standard recombinant methodology and can bind to IL-TIF (undefined). The
CC zcytor16 protein is useful for: inhibiting IL-TIF induced proliferation
CC or differentiation of hematopoietic cell(s) (progenitors); reducing
CC IL-TIF induced or IL-9 induced inflammation; and suppressing an
CC inflammatory response in a mammal with inflammation. Heteromeric/
CC multimeric receptor polypeptides such as soluble zcytor 16/CRF2-4 can be
CC used to reduce progression and symptoms of cancer. Zcytor16 polypeptides
CC can also be used to detect IL-TIF levels which is indicative of
CC pathological conditions including inflammatory states (e.g. rheumatoid
CC arthritis) and cancer. Antibodies that bind zcytor16 polypeptides and the
CC polypeptides themselves are useful for the treatment of inflammation,
CC inflammatory diseases (e.g. infection, asthma, inflammatory bowel
CC disease, rheumatoid arthritis and atherosclerosis) and autoimmune
CC diseases. The antibodies and zcytor16 polynucleotides are also useful
CC for detecting cancer. The present sequence represents a cDNA encoding
CC the human IL-TIF protein.
XX
SQ Sequence 1116 BP; 336 A; 229 C; 222 G; 329 T; 0 other;

Query Match 100.0%; Score 1116; DB 22; Length 1116;
Best Local Similarity 100.0%; Pred. No. 2.9e-233;
Matches 1116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
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Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Db     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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RESULT 3
AAC81773
ID AAC81773 standard; cDNA; 1177 BP.
XX
AC AAC81773;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human GIL-19/AE289 protein coding sequence.
XX
KW Human; GIL-19/AE289; IL-10; interleukin-10; nutrition;
KW cell proliferation; immune stimulation; immune suppression;
KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200065027-A2.
XX
PD 02-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11479.
XX
PR 28-APR-1999; 99US-0131473.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Fouser L, Spaulding V, Xuan D;
XX
DR WPI; 2000-687325/67.
DR P-PSDB; AAB36292.

```
XX
PT   Human GIL-19 protein that shows a high degree of homology to IL
PT   (interleukin)-10, useful in upregulation of humoral immune responses,
PT   as an antiinflammatory agent and as a modulator of immune responses
PT   associated with injury -
XX
PS   Claim 1; Page 59; 60pp; English.
XX
CC   The present invention provides the protein and coding sequences for the
CC   novel human GIL-19/AE289 protein. The protein shows homology to
CC   interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used
CC   in the regulation of cell proliferation and differentiation,
CC   haematopoiesis, immune stimulation or suppression, tissue growth and
CC   tumour inhibition. In addition, it also has uses in the treatment of
CC   inflammation and in nutrition.
XX
SQ   Sequence 1177 BP; 362 A; 245 C; 232 G; 338 T; 0 other;


  Query Match           100.0%;  Score 1116;  DB 21;  Length 1177;
  Best Local Similarity  100.0%;  Pred. No. 3e-233;
  Matches 1116;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db    225 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 284

Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Db    585 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 644

Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Db    645 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 704

Qy    661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    705 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 764

Qy    721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    765 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 824

Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    825 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 884

Qy    841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    885 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 944

Qy    901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    945 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 1004

Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1005 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1064

Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1065 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1124

Qy   1081 tgtttatttgacctcaataaacacttggatatccta 1116
          ||||||||||||||||||||||||||||||||||||
Db   1125 tgtttatttgacctcaataaacacttggatatccta 1160


RESULT   4
AAF92134
ID   AAF92134 standard; cDNA; 1152 BP.
XX
AC   AAF92134;
XX
DT   15-MAY-2001  (first entry)
XX
DE   Human PRO10096 cDNA.
XX
KW   Human; PRO protein; mapping; ss.
XX
OS   Homo sapiens.
XX
PN   WO200116318-A2.
XX
PD   08-MAR-2001.
XX
PF   24-AUG-2000; 2000WO-US23328.
XX
PR   01-SEP-1999;   99WO-US20111.
PR   15-SEP-1999;   99WO-US21090.
PR   07-DEC-1999;   99US-0169495.
PR   09-DEC-1999;   99US-0170262.
PR   11-JAN-2000; 2000US-0175481.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   03-MAR-2000; 2000US-0187202.
PR   25-APR-2000; 2000US-0199397.
PR   22-MAY-2000; 2000WO-US14042.
PR   05-JUN-2000; 2000US-0209832.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Eaton DL,  Filvaroff E,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi CJ,  Gurney AL,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2001-183260/18.
DR   P-PSDB; AAB87602.
XX
PT   Eighty four nucleic acids encoding PRO polypeptides, useful in
PT   molecular biology, including use as hybridization probes, and in
PT   chromosome and gene mapping. -
XX
```

```
PS   Claim 2; Fig 153; 278pp; English.
XX
CC   The present sequence is the coding sequence for a human PRO polypeptide
CC   (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
CC   antagonists or anti-PRO antibodies are useful for preparation of a
CC   medicament useful in the treatment of a condition which is responsive to
CC   the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
CC   protein may also be employed as molecular weight markers for protein
CC   electrophoresis. The PRO coding sequence has applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping.
XX
SQ   Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;


  Query Match             99.8%;  Score 1114;  DB 22;  Length 1152;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-233;
  Matches 1114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 97

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 157

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 217

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 277

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 337

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 397

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 457

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 517

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 577

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 637

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     638 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 697

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     698 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 757

Qy     721 aaccaatgccactttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     758 aaccaatgccactttttgtttataagaccagaaggtagactttctaagcatagatatttat 817

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     818 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 877

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     878 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 937

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     938 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 997

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaaacatcattcgata 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     998 ctgcattttatttatatcattttattaatatggatttatttatagaaaacatcattcgata 1057

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1058 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1117

Qy    1081 tgtttatttgacctcaataaacacttggatatcc 1114
          ||||||||||||||||||||||||||||||||
Db    1118 tgtttatttgacctcaataaacacttggatatcc 1151


RESULT   5
AAC87053
ID   AAC87053 standard; cDNA; 1152 BP.
XX
AC   AAC87053;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of human polypeptide PRO10096.
XX
KW   Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;
KW   PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;
KW   PRO1183; PRO1272; PRO1419; PRO4999; PRO7170; PRO248; PRO353; PRO1318;
KW   PRO1600; PRO9940; PRO533; PRO301; PRO187; PRO337; PRO1411; PRO4356;
KW   PRO246; PRO265; PRO941; PRO10096; PRO6003; PRO6004; PRO350; PRO2630;
KW   PRO6309; cell death; genetic disorder; transgenic animal; gene therapy;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             58..597
FT                   /*tag=  a
FT   sig_peptide     58..156
FT                   /*tag=  b
XX
PN   WO200077037-A2.
XX
PD   21-DEC-2000.
XX
PF   22-MAY-2000; 2000WO-US14042.
XX
PR   15-JUN-1999;   99US-0139695.
PR   20-JUL-1999;   99US-0145070.
PR   26-JUL-1999;   99US-0145698.
PR   17-AUG-1999;   99US-0149396.
PR   01-SEP-1999;   99WO-US20111.
PR   08-SEP-1999;   99WO-US20594.
PR   15-SEP-1999;   99WO-US21090.
PR   15-SEP-1999;   99WO-US21547.
PR   30-NOV-1999;   99WO-US28313.
PR   01-DEC-1999;   99WO-US28301.
PR   02-DEC-1999;   99WO-US28565.
PR   07-DEC-1999;   99US-0169495.
PR   05-JAN-2000; 2000WO-US00219.
PR   18-FEB-2000; 2000WO-US04341.
PR   18-FEB-2000; 2000WO-US04342.
PR   22-FEB-2000; 2000WO-US04414.
PR   01-MAR-2000; 2000WO-US05601.
PR   02-MAR-2000; 2000WO-US05841.
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PR   20-MAR-2000; 2000WO-US07377.
PR   30-MAR-2000; 2000WO-US08439.
PR   15-MAY-2000; 2000WO-US13358.
PR   17-MAY-2000; 2000WO-US13705.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Botstein DA,  Desnoyers L,  Eaton DL;
PI   Ferrara N,  Fong S,  Gao W,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Kljavin IJ,  Mather JP,  Napier MA,  Pan J;
PI   Paoni NF,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK,  Williams PM;
PI   Wood WI,  Zhang Z;
XX
DR   WPI; 2001-050091/06.
DR   P-PSDB; AAB31210.
XX
PT   Isolated nucleic acid molecule encoding a PRO polypeptide which is a
PT   transmembrane polypeptide is useful for gene therapy and identification
PT   of related polypeptides -
XX
PS   Claim 2; Fig 63; 244pp; English.
XX
CC   The present sequence encodes a human secreted and transmembrane
CC   polypeptide. The specification describes human polypeptides, designated
CC   PRO196, PRO444, PRO183, PRO185, PRO210, PRO215, PRO217, PRO242, PRO288,
CC   PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO4999, PRO7170,
CC   PRO248, PRO353, PRO1318, PRO1600, PRO9940, PRO533, PRO301, PRO187,
CC   PRO337, PRO1411, PRO4356, PRO246, PRO265, PRO941, PRO10096, PRO6003,
CC   PRO6004, PRO350, PRO2630 and PRO6309. The biological activity of cells
CC   can be modulated with agents that bind to these polypeptides, resulting
CC   in the death of the cells. The polynucleotides encoding these
CC   polypeptides are useful in the recombinant production of the
CC   polypeptides, as a hybridisation probe to screen libraries to isolate
CC   homologous sequences, or to map the gene. They may also be used for
CC   analysing genetic disorders, and to produce transgenic animals which are
CC   useful for the development and screening of therapeutically useful
CC   reagents. The polynucleotides can also be used in gene therapy e.g. to
CC   replace a defective gene.
XX
SQ   Sequence 1152 BP; 342 A; 244 C; 228 G; 338 T; 0 other;
```

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  Query Match             99.8%;  Score 1114;  DB 22;  Length 1152;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-233;
  Matches 1114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      38 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 97

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      98 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 157

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 217

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 277

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 337

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     338 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 397

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 457

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 517

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     518 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 577

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     578 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccctttcc 637

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     638 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 697

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     698 aagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaagga 757

Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     758 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 817

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Db     818 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 877

Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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Db     878 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 937

Qy     901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     938 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 997

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     998 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1057

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1058 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1117

Qy    1081 tgtttatttgacctcaataaacacttggatatcc 1114
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Db    1118 tgtttatttgacctcaataaacacttggatatcc 1151
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```
RESULT   6
AAF28841
ID   AAF28841 standard; DNA; 1139 BP.
XX
AC   AAF28841;
XX
DT   25-APR-2001  (first entry)
XX
DE   Human interleukin-10 homologue IL-D110 DNA sequence.
XX
KW   Anti-inflammatory; immunosuppressive; cytostatic; antirheumatic; human;
KW   antiarthritic; dermatological; thyromimetic; gene therapy; inflammation;
KW   interleukin 10 homologue; IL-D110; IL-D210; cytokine; tumour therapy;
KW   haematopoietic cell; probe; immunogen; systemic lupus erythematosus;
KW   rheumatoid arthritis; Hashimoto's autoimmune response; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= "IL-D110"
FT                   /transl_except= (pos:245..247,aa:Xaa)
```

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FT                   /note= "Xaa=unknown"
FT   sig_peptide     59..157
FT                   /*tag= b
FT   mat_peptide     158..595
FT                   /*tag= c
XX
PN   WO200073457-A1.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14729.
XX
PR   27-MAY-1999;   99US-0322806.
XX
PA   (SCHE ) SCHERING CORP.
XX
PI   Parham CL,  De Waal Malefyt R,  Marehalli NL;
XX
DR   WPI; 2001-061539/07.
DR   P-PSDB; AAB37122.
XX
PT   New interleukin-D110 genes and polypeptides useful for treating
PT   conditions associated with abnormal physiology, particularly e.g.
PT   inflammatory or autoimmune disorders -
XX
PS   Claim 3; Page 51-52; 62pp; English.
XX
CC   This sequence represents the gene sequence for a human interleukin 10
CC   homologue IL-D110. The invention also relates to another IL-10 homologue
CC   ID-210 (AAF28842). The IL-D110 is useful for treating conditions
CC   associated with abnormal physiology or development, including
CC   inflammatory conditions, either acute or chronic. The new cytokine
CC   also plays a role in the regulation or development of haematopoietic
CC   cells, e.g. lymphoid or myeloid cells, which affect immunological
CC   responses, such as inflammation and/or autoimmune disorders. These may
CC   also be used in drug screening to identify compounds having binding
CC   affinity to or other relevant biological effects on IL-D110 functions,
CC   in anti-tumour therapy, as probes for detecting IL-D110 levels in samples
CC   from patients suspected of having an abnormal condition, e.g. autoimmune
CC   or inflammatory, in raising or screen antibodies, as immunogen, in
CC   diagnostic assays, and in detecting, isolating or identifying a DNA clone
CC   encoding IL-D110 or IL-D210 from a natural source. IL-D110 antagonists
CC   may be used to block immune responses, e.g. in situations as inflammatory
CC   or autoimmune responses, including rheumatoid arthritis, systemic lupus
CC   erythematosus, or Hashimoto's autoimmune responses.
XX
SQ   Sequence 1139 BP; 337 A; 238 C; 227 G; 333 T; 4 other;
```

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  Query Match             98.3%;  Score 1096.6;  DB 22;  Length 1139;
  Best Local Similarity   99.5%;  Pred. No. 4.9e-229;
  Matches 1096;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      39 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 98

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
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Db      99 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 158

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db     159 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 218

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Db     219 accgcaccttcatgctggctaaggaggntagcttggctgataacaacacagacgttcgtc 278

Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     279 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 338

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     339 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 398

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     399 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 458

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     519 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 578

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     579 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 638

Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     639 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 698

Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:
Db     699 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaaggr 758

Qy     721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
           ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db     759 aaccaatgccacttttgtttataagaccagaaggtagactttctwagcatagatatttat 818

Qy     781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Qy     841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     879 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 938

Qy     901 gcttcatgtttccataatcagtactttatatttataaaatgtatttattattattataaga 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     939 gcttcatgtttccataatcagtactttatatttataaaatgtatttattattattataaga 998

Qy     961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     999 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1058

Qy    1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1059 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1118

Qy    1081 tgtttatttgacctcaataaa 1101
           ||||||| |||||||||| ||
Db    1119 tgtttatntgacctcaatgaa 1139
```

```
RESULT   7
AAC84310
ID   AAC84310 standard; cDNA; 1132 BP.
XX
AC   AAC84310;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human EXCS encoding cDNA (clone ID 5571181CB1).
XX
KW   Extracellular signaling molecule; EXCS; anti-inflammatory; human;
KW   immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
KW   virucide; antibacterial; anti-HIV; human immunodeficiency virus;
KW   antiinfertility; cerebroprotective; nootropic; antiulcer; antifungal;
KW   anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
KW   keratolytic; protozoacide; gene therapy; ss.
```

XX
OS Homo sapiens.
XX
PN WO200070049-A2.
XX
PD 23-NOV-2000.
XX
PF 19-MAY-2000; 2000WO-US13975.
XX
PR 19-MAY-1999; 99US-0134949.
PR 15-JUL-1999; 99US-0144270.
PR 30-JUL-1999; 99US-0146700.
PR 04-OCT-1999; 99US-0157508.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
PI Azimzai Y, Lu DAM, Patterson C;
XX
DR WPI; 2001-025021/03.
DR P-PSDB; AAB48074.
XX
PT New human extracellular signaling nucleic acids and polypeptides useful
PT for diagnosing, treating and preventing infections and
PT gastrointestinal, neurological, reproductive, and
PT autoimmune/inflammatory disorders -
XX
PS Claim 4; Page 108; 114pp; English.
XX
CC The invention provides human extracellular signaling molecules (EXCS)
CC and polynucleotides which identify and encode EXCS. EXCS can be
CC expressed by standard recombinant methodology. The amino acid and nucleic
CC acid sequences of EXCS are useful for diagnosing, treating and
CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,
CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular
CC disease, stroke), reproductive (infertility, ovulatory defects,
CC endometriosis), autoimmune /inflammatory (actinic keratosis, acquired
CC immunodeficiency syndrome (AIDS), Addison's disease), and cell
CC proliferative disorders including cancers (of the breast, adrenal gland,
CC bone). They may also be used to treat fatal familial insomnia,
CC nutritional and metabolic diseases of the nervous system, myopathies,
CC mental disorders (anxiety, schizophrenia, mood), as well as infections
CC caused by parasites (malaria, leishmania, trypanosoma), viral
CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,
CC staphylococcus, bacillus), and fungal (aspergillus, blastomyces,
CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,
CC agonists, pharmaceutical compositions, and antibodies may also be used
CC for treating or preventing disorders associated with increased or
CC decreased expression or activity of EXCS. EXCS polynucleotides may also
CC be used to detect and quantify gene expression in biopsied tissues in
CC which expression of EXCS may be correlated with the disease, to determine
CC presence or excess expression of EXCS, to monitor regulation of EXCS
CC levels during therapeutic intervention, to detect the presence of
CC associated disorders, as targets in microarray, to generate hybridization
CC probes, and to detect differences in gene sequences among normal, carrier
CC or affected individuals. Antibodies may also be used in diagnosing
CC disorders, in monitoring patients being treated with EXCS agonists,
CC antagonists or inhibitors. Sequences AAC84293-C84318 represent nucleic
CC acid molecules encoding the EXCS of the invention.
XX
SQ Sequence 1132 BP; 333 A; 240 C; 226 G; 333 T; 0 other;

Query Match 97.7%; Score 1090.4; DB 22; Length 1132;
Best Local Similarity 99.9%; Pred. No. 1.1e-227;
Matches 1091; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
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Db     31 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 90

Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
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Db     91 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 150

Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 210

Qy    181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 270

Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Db    391 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 450

Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 510

Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 570

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttcc 630

Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 690

Qy    661 aagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaagga 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 aagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaagga 750

Qy    721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 810

Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Db    811 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 870

Qy    841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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Db    871 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 930

Qy    901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Db    931 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 990

Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Qy   1081 tgtttatttgac 1092
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Db   1111 tgtttatttgcc 1122
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RESULT 8
AAA28839

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ID   AAA28839 standard; cDNA; 690 BP.
XX
AC   AAA28839;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Human T cell inducible factor cDNA.
XX
KW   TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW   Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist;
KW   probe; chromosome 12q15; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             72..611
FT                   /*tag= a
XX
PN   WO200024758-A1.
XX
PD   04-MAY-2000.
XX
PF   18-OCT-1999;   99WO-US24424.
XX
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Dumoutier L,  Louhed J,  Renauld J;
XX
DR   WPI; 2000-422495/36.
DR   P-PSDB; AAY92879.
XX
PT   New nucleic acid molecule encoding a T cell derived inducible factor
PT   for treating asthma, an allergy or lymphoma
XX
PS   Claim 1; Page 38; 46pp; English.
XX
CC   This cDNA encodes a human T cell derived inducible factor (TIF). The gene
CC   was mapped to chromosome 12q15. The human TIF was identified based on
CC   homology to a murine TIF, which was identified by subtraction cloning
CC   from a murine lymphoma cell line BW5147 in the presence or absence of
CC   interleukin 9 (IL-9). BW5147, can be grown in vitro, without the need to
CC   add any cytokines to its culture medium. Many IL-9 activities are
CC   mediated by activation of STAT transcription factors. The novel TIFs were
CC   expressed in the presence of IL-9, but not in its absence. TIFs induce
CC   STAT activation in cells. They can be used, e.g. in the stimulation of
CC   regeneration of targeted tissues. Their inhibitors or antagonists can be
CC   used to retard, prevent or inhibit differentiation of other tissues. The
CC   TIFs and their coding sequences are useful in the treatment of asthma,
CC   allergies and lymphoma (claimed). They are also useful for identifying
CC   compounds that inhibit or activate T cell induced factor activity in a
CC   cell (claimed).
XX
SQ   Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

  Query Match             57.3%;  Score 639;  DB 21;  Length 690;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-129;
  Matches  639;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
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Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Db     292 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 351

Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Db     352 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 411

Qy     361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Db     412 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 471

Qy     421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Db     472 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 531

Qy     481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Db     532 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 591

Qy     541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 600
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Db     592 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 651

Qy     601 ctgctagaaataacaattagatgccccaaagcgattttt 639
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Db     652 ctgctagaaataacaattagatgccccaaagcgattttt 690


RESULT   9
AAS14875
ID   AAS14875 standard; cDNA; 690 BP.
XX
AC   AAS14875;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Human cDNA encoding T cell derived inducible factor, TIF.
XX
KW   Human; T cell derived inducible factor; TIF; ss; antiallergic;
KW   antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW   cancer; lymphoma; immune system disorder; allergy; asthma;
KW   acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW   thyroiditis; melanoma; hepatoma.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "TIF"
FT                   /transl_except= (pos:159..161,aa:Glu)
FT                   /transl_except= (pos:378..380,aa:Ile)
FT                   /transl_except= (pos:405..407,aa:Arg)
FT                   /transl_except= (pos:519..521,aa:Cys)
XX
PN   US2001024652-A1.
XX
PD   27-SEP-2001.
XX
PF   29-DEC-2000; 2000US-0751797.
XX
PR   18-OCT-1999;   99US-0419568.
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (DUMO/) DUMOUTIER L.
PA   (LOUA/) LOUAHED J.
```

PA (RENA/) RENAULD J.
XX
PI Dumoutier L, Louahed J, Renauld J;
XX
DR WPI; 2001-638496/73.
DR P-PSDB; AAU09091.
XX
PT New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy -
XX
PS Claim 1; Page 17; 26pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their muteins) may be used to test IL-9
CC ant/agonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence encodes human TIF.
XX
SQ Sequence 690 BP; 182 A; 176 C; 167 G; 165 T; 0 other;

Query Match 57.3%; Score 639; DB 22; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.3e-129;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Db    232 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 291

Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    292 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 351

Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    352 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 411

Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    412 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 471

Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    472 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 531

Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    532 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 591

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    592 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttttcc 651

Qy    601 ctgctagaaataacaattagatgccccaaagcgattttt 639
          |||||||||||||||||||||||||||||||||||||||
```

Db 652 ctgctagaaataacaattagatgccccaaagcgattttt 690

RESULT 10
AAC81774
ID AAC81774 standard; cDNA; 1166 BP.
XX
AC AAC81774;
XX
DT 23-FEB-2001 (first entry)
XX
DE Murine GIL-19 protein coding sequence.
XX
KW Mouse; GIL-19/AE289; IL-10; interleukin-10; nutrition;
KW cell proliferation; immune stimulation; immune suppression;
KW haematopoiesis regulation; tissue growth; inflammation; cancer; ss.
XX
OS Mus sp.
XX
PN WO200065027-A2.
XX
PD 02-NOV-2000.
XX
PF 28-APR-2000; 2000WO-US11479.
XX
PR 28-APR-1999; 99US-0131473.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Fouser L, Spaulding V, Xuan D;
XX
DR WPI; 2000-687325/67.
XX
PT Human GIL-19 protein that shows a high degree of homology to IL
PT (interleukin)-10, useful in upregulation of humoral immune responses,
PT as an antiinflammatory agent and as a modulator of immune responses
PT associated with injury -
XX
PS Disclosure; Fig 1; 60pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC novel human GIL-19/AE289 protein. The protein shows homology to
CC interleukin-10 (IL-10) and is assumed to be a cytokine. It can be used
CC in the regulation of cell proliferation and differentiation,
CC haematopoiesis, immune stimulation or suppression, tissue growth and
CC tumour inhibition. In addition, it also has uses in the treatment of
CC inflammation and in nutrition.
XX
SQ Sequence 1166 BP; 375 A; 241 C; 244 G; 306 T; 0 other;

Query Match 47.1%; Score 526; DB 21; Length 1166;
Best Local Similarity 74.4%; Pred. No. 5.7e-105;
Matches 820; Conservative 0; Mismatches 245; Indels 37; Gaps 11;

```
Qy     15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74
          |||   ||||| | ||||||||||||||| |||| | || ||||||||||||  ||||| ||
Db     69 tctctgatggctgtcctgcagaaatctatgagtttttcccttatggggactttggccgcc 128

Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
          |||||||| |||||| | ||||| | ||  ||||  | |   ||   |||| ||| | ||
Db    129 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccgtcaacacc 188

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
          |  |||| ||||||   |||||||||||||||||| || |||  |||||||||||| |||
Db    189 cggtgcaagcttgaggtgtccaacttccagcagccatacatcgtcaaccgcacctttatg 248

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
          ||||| |||||||| ||| | || ||||||||||||||| || || ||||| |||||||||
Db    249 ctggccaaggaggccagccttgcagataacaacacagatgtccggctcatcggggagaaa 308

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
          |||||||  |||||||||   |  || |  ||||| ||||||||||||||||| ||||||
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```
Db    309 ctgttccgaggagtcagtgctaaggatcagtgctacctgatgaagcaggtgctcaacttc 368

Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
          ||||| ||||| || ||| |||| || || || |||||||||||| || ||||||||||||
Db    369 accctggaagacgttctgctcccccagtcagacaggttccagccctacatgcaggaggtg 428

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
          ||||| |||||| ||| |||||||||   ||| ||| | ||||| ||    ||||| |||
Db    429 gtgcctttcctgaccaaactcagcaatcagctcagctcctgtcacatcagcggtgacgac 488

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
          | | | ||||||| ||||||   || |||||||||| ||||||||||||||||||||||||
Db    489 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagt 548

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
          |||||||||||| || ||||| ||||||||  ||||||||||||||||||||||||| |||
Db    549 ggagagatcaaggcgattggggaactggacctgctgtttatgtctctgagaaatgcttgc 608

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttccctgctagaaataac 614
            | ||| |      |||||  |||| ||| ||||    ||    | ||| ||| ||| |||
Db    609 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 668

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
          ||| |||| ||  || |   ||||||     | |||||||  || ||||| ||  |||||
Db    669 aataagatccctgaatggacttttta----ctaaaggaaagtgagaagctaacgtccat 724

Qy    675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccactt 734
          ||| ||  |  |||| || ||||| ||  ||     | | |||| |||      | |
Db    725 cattattagaagatttcacatgaaacctggctcagttgaaaaagaaaatagtgtcaa--g 782

Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
          ||||  || ||||||| |||||||||  ||| || | | ||| ||||| || |||| ||
Db    783 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 841

Qy    795 tgtaactggtgttctatacacagaaaacaatttatttttttaaataattgtctttttccat 854
          ||| |||| ||    |||||    ||| |   | |  |||||| |||||| |
Db    842 tgtcactgatg----atacaacagaaaaataatgtactttaaaaaattgttt-------g 890

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttcca 914
          |||  || |||| |  ||||||||||   |||||||  | ||  || |||||  ||||||
Db    891 aaaggaggttacctctcattccttta---gaaaaaaagcttatgtaacttca--tttcca 945

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
          ||| || || ||||||| | ||| | ||||||||||| | ||||      ||||||||||
Db    946 taaccaatattttatatatgtaagtttatttattataagtata------cattttattta 999

Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
          | ||| ||||||||||||||||||||||||||||||||| ||  | |||||| || || |||
Db   1000 tgtcagtttattaatatggatttatttatagaaacattatctgctattgata-tttagta 1058

Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
          ||||||| ||||   |||||||||||||||| ||| |    | |  | | || | | |
Db   1059 taaggcaaata---atatttatgacaataactatgg----aaacaagatatcttaggctt 1111

Qy   1095 caataaacacttggatatccta 1116
            |||||||| ||||||||  ||
Db   1112 taataaacacatggatatcata 1133
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RESULT 11
AAA28817
ID   AAA28817 standard; cDNA; 1111 BP.
XX
AC   AAA28817;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Murine T cell inducible factor beta cDNA.
XX
KW   TIF-beta; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW   Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             50..589
FT                   /*tag=  a
XX
PN   WO200024758-A1.
XX
PD   04-MAY-2000.
XX
PF   18-OCT-1999;   99WO-US24424.
XX
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Dumoutier L,  Louhed J,  Renauld J;
XX
DR   WPI; 2000-422495/36.
DR   P-PSDB; AAY92878.
XX
PT   New nucleic acid molecule encoding a T cell derived inducible factor
PT   for treating asthma, an allergy or lymphoma
XX
PS   Claim 1; Page 33-34; 46pp; English.
XX
CC   This cDNA encodes T cell derived inducible factor (TIF) beta identified
CC   by subtraction cloning from a murine lymphoma cell line BW5147 in the
CC   presence or absence of interleukin 9 (IL-9). There was a great deal of
CC   homology with TIF-alpha cDNA (AAA28815). The main difference was that
CC   the promoters where not homologous suggesting independent regulation.
CC   BW5147, can be grown in vitro, without the need to add any cytokines to
CC   its culture medium. Many IL-9 activities are mediated by activation of
CC   STAT transcription factors. The novel TIFs were expressed in the presence
CC   of IL-9, but not in its absence. TIFs induce STAT activation in cells.
CC   They can be used, e.g. in the stimulation of regeneration of targeted
CC   tissues. Their inhibitors or antagonists can be used to retard, prevent
CC   or inhibit differentiation of other tissues. The TIFs and their coding
CC   sequences are useful in the treatment of asthma, allergies and lymphoma
CC   (claimed). They are also useful for identifying compounds that inhibit or
CC   activate T cell induced factor activity in a cell (claimed).
XX
SQ   Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;
```

```
  Query Match             47.1%;  Score 525.2;  DB 21;  Length 1111;
  Best Local Similarity   73.8%;  Pred. No. 8.3e-105;
  Matches  813;  Conservative    0;  Mismatches  253;  Indels   36;  Gaps   10;

Qy      15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74
           || |  ||||| | |||||||||||||| |||| | || ||||||||||||  ||||| ||
Db      44 tcggtgatggctgtcctgcagaaatctatgagtttttcccttatggggactttggccgcc 103

Qy      75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
           |||||||| |||||| | ||||| | ||  |||| | |   ||  |||||||| | ||
Db     104 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccatcaacacc 163

Qy     135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
           |  |||| ||||||   |||||||||||||||||| || |||  ||||||||||| |||
Db     164 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 223

Qy     195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
           ||||| |||||||| ||| | || |||||||||||||||| || ||||| |||||||||
Db     224 ctggccaaggaggccagccttgcagataacaacacagacgtccggctcatcggggagaaa 283

Qy     255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
           |||||||  |||||||||   | || | |||||  ||||||||||||||||||  ||||||
Db     284 ctgttccgaggagtcagtgctaaggatcagtgctacctgatgaagcaggtgctcaacttc 343

Qy     315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
           ||||| |||||  | ||| |||| || || || ||||||| ||| || ||||||||||||
Db     344 accctggaagacattctgctcccccagtcagacaggttccggccctacatgcaggaggtg 403
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Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
          ||||| |||||| ||| |||||||||   ||| ||| | ||||| ||    ||||| |||
Db    404 gtgcctttcctgaccaaactcagcaatcagctcagctcctgtcacatcagtggtgacgac 463

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
          | | | ||||||| ||||||   || |||||||| ||||||||||||||||||||||||
Db    464 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagc 523

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
          |||||||||||||| || || |||||||| ||||||||||||||||||||||||||| |||
Db    524 ggagagatcaaagcgatcggggaactggacctgctgtttatgtctctgagaaatgcttgc 583

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaaccccctttccctgctagaaataac 614
          | ||| |      ||||| |||| ||| ||||   ||    | ||| ||| ||| |||
Db    584 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 643

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
          ||| |||| ||  || |   ||||||     | |||||||  || ||||| ||  ||||
Db    644 aataagatccctgaatggacttttta----ctaaaggaaagtgagaagctaacgtccac 699

Qy    675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccactt 734
          ||| ||  |  |||| || ||||| ||  ||     | | | || |||      | |
Db    700 catcattagaagatttcacatgaaacctggctcagttgaaagagaaaatagtgtcaa--g 757

Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
          ||||  || ||||||| |||||||||||  ||| || | | ||| ||||| || |||| ||
Db    758 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 816

Qy    795 tgtaactggtgttctatacacagaaaacaatttatttttttaaataattgtctttttccat 854
          ||| | || |     || ||    ||| | | | |  |||||| |||||| |
Db    817 tgtcattgat----aatgcaacagaaaaagtatgtactttaaaaaattgttt-------g 865

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttcca 914
          |||  || |||| |  |||||| ||   ||| |||  ||||  || |||||  ||||||
Db    866 aaaggaggttacctctcattcctcta---gaagaaaagcctatgtaacttca--tttcca 920

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
          ||| || |||||||||| | ||| | |||||||||| | ||||      ||||||||||
Db    921 taaccaatactttatatatgtaagtttatttattataagtata------cattttattta 974

Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
          | ||| ||||||||||||||||||||||||||| || ||  ||| ||| || ||||||
Db    975 tgtcagtttattaatatggatttatttatagaaaaattatctgatgttgatatttgagta 1034

Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
          ||| || ||||   |||||||||| ||||| |||||    | |  |  | | || | | |
Db   1035 taaagcaaata---atatttatgataataactatag----aaacaagatatcttaggctt 1087

Qy   1095 caataaacacttggatatccta 1116
            ||||||||| || ||||| ||
Db   1088 taataaacacatgaatatcata 1109
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RESULT 12
AAS14860
ID AAS14860 standard; cDNA; 1111 BP.
XX
AC AAS14860;
XX
DT 19-DEC-2001 (first entry)
XX
DE Mouse cDNA for T cell derived inducible factor, TIFbeta.
XX
KW Mouse; T cell derived inducible factor; TIFbeta; ss; antiallergic;
KW antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW cancer; lymphoma; immune system disorder; allergy; asthma;
KW acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW thyroiditis; melanoma; hepatoma.
XX
OS Mus musculus.
XX
PN US2001024652-A1.
XX
PD 27-SEP-2001.
XX
PF 29-DEC-2000; 2000US-0751797.
XX
PR 18-OCT-1999; 99US-0419568.
PR 26-OCT-1998; 98US-0178973.
PR 16-JUL-1999; 99US-0354243.
XX
PA (DUMO/) DUMOUTIER L.
PA (LOUA/) LOUAHED J.
PA (RENA/) RENAULD J.
XX
PI Dumoutier L, Louahed J, Renauld J;
XX
DR WPI; 2001-638496/73.
XX
PT New isolated nucleic acid molecules encoding T cell inducible factors,
PT useful as markers for expression or effect of interleukin (IL)-9 in a
PT subject and diagnosing susceptibility to asthma or allergy
XX
PS Claim 1; Page 14; 26pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule, which encodes
CC a T cell derived inducible factor (TIF) which are upregulated by the
CC cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC activation. The TIF proteins (or their muteins) may be used to test IL-9
CC ant/agonists for their potency against lymphomas, immune system
CC disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC or inhibit differentiation of tissue types in which they are active and
CC therefore be used to develop treatments for melanomas and hepatomas.
CC The present sequence is a cDNA for mouse TIFbeta.
XX
SQ Sequence 1111 BP; 346 A; 232 C; 236 G; 297 T; 0 other;

Query Match 47.1%; Score 525.2; DB 22; Length 1111;
Best Local Similarity 73.8%; Pred. No. 8.3e-105;
Matches 813; Conservative 0; Mismatches 253; Indels 36; Gaps 10;

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Qy     15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74
          || |  ||||| | |||||||||||||| |||| | || ||||||||||||  ||||| ||
Db     44 tcggtgatggctgtcctgcagaaatctatgagtttttcccttatggggactttggccgcc 103

Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
          |||||||| |||||| | ||||| | ||  ||||  | |   ||   |||||||| | ||
Db    104 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccatcaacacc 163

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
          |  |||| ||||||   |||||||||||||||||| || |||  |||||||||||| |||
Db    164 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 223

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
          ||||| |||||||| ||| | || ||||||||||||||||| || ||||| |||||||||
Db    224 ctggccaaggaggccagccttgcagataacaacacagacgtccggctcatcggggagaaa 283

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
          |||||||  |||||||||   |  || |  ||||| ||||||||||||||||| ||||||
Db    284 ctgttccgaggagtcagtgctaaggatcagtgctacctgatgaagcaggtgctcaacttc 343

Qy    315 accettgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
          ||||| |||||  | ||| |||| || || || ||||||| ||| || ||||||||||||
Db    344 accctggaagacattctgctcccccagtcagacaggttccggccctacatgcaggaggtg 403

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
          ||||| |||||| |||  ||||||||   ||| ||| | ||||| ||    ||||| |||
Db    404 gtgcctttcctgaccaaactcagcaatcagctcagctcctgtcacatcagtggtgacgac 463

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
          | | | ||||||| ||||||   || |||||||| ||||||||||||||||||||||||
Db    464 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagc 523

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
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Db    524 ggagagatcaaagcgatcggggaactggacctgctgtttatgtctctgagaaatgcttgc 583

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttccctgctagaaataac 614

Db    584 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 643

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674

Db    644 aataagatccctgaatggacttttta----ctaaaggaaagtgagaagctaacgtccac 699

Qy    675 catgatgggtggattccaaatgaaccccctgcgttagttacaaaggaaaccaatgccactt 734

Db    700 catcattagaagatttcacatgaaacctggctcagttgaaagagaaaatagtgtcaa--g 757

Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794

Db    758 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 816

Qy    795 tgtaactggtgttctatacacagaaaacaatttatttttttaaataattgtctttttccat 854

Db    817 tgtcattgat----aatgcaacagaaaaagtatgtactttaaaaaattgttt-------g 865

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttcca 914

Db    866 aaaggaggttacctctcattcctcta---gaagaaaagcctatgtaacttca--tttcca 920

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974

Db    921 taaccaatactttatatatgtaagtttatttattataagtata------cattttattta 974

Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034

Db    975 tgtcagtttattaatatggatttatttatagaaaaattatctgatgttgatatttgagta 1034

Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094

Db   1035 taaagcaaata---atatttatgataataactatag----aaacaagatatcttaggctt 1087

Qy   1095 caataaacacttggatatccta 1116

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RESULT  13
AAA28815
ID   AAA28815 standard; cDNA; 1119 BP.
XX
AC   AAA28815;
XX
DT   04-SEP-2000  (first entry)
XX
DE   Murine T cell inducible factor alpha cDNA.
XX
KW   TIF-alpha; T cell derived inducible factor; interleukin 9; STAT; IL-9;
KW   Anti-asthmatic; anti-allergic; cytostatic; inhibitor; antagonist; ss.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             52..591
FT                   /*tag=  a
XX
PN   WO200024758-A1.
XX
PD   04-MAY-2000.
XX
PF   18-OCT-1999;   99WO-US24424.
XX
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Dumoutier L,  Louhed J,  Renauld J;
XX
DR   WPI; 2000-422495/36.
DR   P-PSDB; AAY92877.
XX
PT   New nucleic acid molecule encoding a T cell derived inducible factor
PT   for treating asthma, an allergy or lymphoma
XX
PS   Claim 1; Page 33; 46pp; English.
XX
CC   This cDNA encodes T cell derived inducible factor (TIF) alpha identified
CC   by subtraction cloning from a murine lymphoma cell line BW5147 in the
CC   presence or absence of interleukin 9 (IL-9). BW5147, can be grown in
CC   vitro, without the need to add any cytokines to its culture medium. Many
CC   IL-9 activities are mediated by activation of STAT transcription
CC   factors. The novel TIFs were expressed in the presence of IL-9, but not
CC   in its absence. TIFs induce STAT activation in cells. They can be used,
CC   e.g. in the stimulation of regeneration of targeted tissues. Their
CC   inhibitors or antagonists can be used to retard, prevent or inhibit
CC   differentiation of other tissues. The TIFs and their coding sequences are
CC   useful in the treatment of asthma, allergies and lymphoma (claimed). They
CC   are also useful for identifying compounds that inhibit or activate T cell
CC   induced factor activity in a cell (claimed).
XX
SQ   Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;
```

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  Query Match             47.0%;  Score 524.4;  DB 21;  Length 1119;
  Best Local Similarity   74.3%;  Pred. No. 1.2e-104;
  Matches  819;  Conservative    0;  Mismatches  246;  Indels   37;  Gaps   11;

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Db     46 tctctgatggctgtcctgcagaaatctatgagttttttcccttatggggactttggccgcc 105

Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134

Db    106 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccgtcaacacc 165

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194

Db    166 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 225

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254

Db    226 ctggccaaggaggccagccttgcagataacaacacagacgtccggctcatcggggagaaa 285

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314

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Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374

Db    346 accctggaagacgttctgctcccccagtcagacaggttccagccctacatgcaggaggtg 405

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434

Db    406 gtaccttcctgaccaaactcagcaatcagctcagctcctgtcacatcagcggtgacgac 465

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494

Db    466 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagt 525

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554

Db    526 ggagagatcaaggcgattggggaactggacctgctgtttatgtctctgagaaatgcttgc 585

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttccctgctagaaataac 614

Db    586 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 645

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
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Db    646 aataagatccctgaatggacttttta----ctaaaggaaagtgagaagctaacgtccat 701

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Db    702 catcattagaagatttcacatgaaacctggctcagttgaaaaagaaaatagtgtcaa--g 759

Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794

Db    760 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 818

Qy    795 tgtaactggtgttctatacacagaaaacaatttatttttttaaataattgtctttttccat 854

Db    819 tgtcactgatg----atacaacagaaaaataatgtactttaaaaaattgttt-------g 867

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccctaaatagcttcatgtttcca 914

Db    868 aaaggaggttacctctcattccttta---gaaaaaaagcttatgtaacttca--tttcca 922

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974

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Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094

Db   1036 taaggcaaata---atatttatgacaataactatgg----aaacaagatatcttaggctt 1088

Qy   1095 caataaacacttggatatccta 1116

Db   1089 taataaacacatggatatcata 1110
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RESULT  14
AAS14858
ID   AAS14858 standard; cDNA; 1119 BP.
XX
AC   AAS14858;
XX
DT   19-DEC-2001  (first entry)
XX
DE   Mouse cDNA encodingT cell derived inducible factor, TIFalpha.
XX
KW   Mouse; T cell derived inducible factor; TIFalpha; ss; antiallergic;
KW   antiasthmatic; cytokine; interleukin-9; IL-9; STAT transcription factor;
KW   cancer; lymphoma; immune system disorder; allergy; asthma;
KW   acquired immunodeficiency syndrome; AIDS; autoimmune diabetes;
KW   thyroiditis; melanoma; hepatoma.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             52..591
FT                   /*tag=  a
FT                   /product= "TIFalpha"
FT   primer_bind     106..126
FT                   /*tag=  b
FT                   /note= "PCR primer appearing as AAS14861"
FT   primer_bind     complement (764..784)
FT                   /*tag=  c
FT                   /note= "PCR primer appearing as AAS14862"
XX
PN   US2001024652-A1.
XX
PD   27-SEP-2001.
XX
PF   29-DEC-2000; 2000US-0751797.
XX
PR   18-OCT-1999;   99US-0419568.
PR   26-OCT-1998;   98US-0178973.
PR   16-JUL-1999;   99US-0354243.
XX
PA   (DUMO/) DUMOUTIER L.
PA   (LOUA/) LOUAHED J.
PA   (RENA/) RENAULD J.
XX
PI   Dumoutier L,  Louahed J,  Renauld J;
XX
DR   WPI; 2001-638496/73.
DR   P-PSDB; AAU09090.
XX
PT   New isolated nucleic acid molecules encoding T cell inducible factors,
PT   useful as markers for expression or effect of interleukin (IL)-9 in a
PT   subject and diagnosing susceptibility to asthma or allergy  -
XX
PS   Claim 1; Page 10; 26pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule, which encodes
CC   a T cell derived inducible factor (TIF) which are upregulated by the
CC   cytokine interleukin-9 (IL-9) and induce STAT transcription factor
CC   activation. The TIF proteins (or their muteins) may be used to test IL-9
CC   ant/agonists for their potency against lymphomas, immune system
CC   disorders, allergies, asthma, acquired immunodeficiency syndrome (AIDS),
CC   autoimmune diabetes and thyroiditis. TIF molecules promote regeneration
CC   or inhibit differentiation of tissue types in which they are active and
CC   therefore be used to develop treatments for melanomas and hepatomas.
CC   The present sequence encodes mouse TIFalpha.
XX
SQ   Sequence 1119 BP; 352 A; 233 C; 232 G; 302 T; 0 other;
```

```
  Query Match             47.0%;  Score 524.4;  DB 22;  Length 1119;
  Best Local Similarity   74.3%;  Pred. No. 1.2e-104;
  Matches  819;  Conservative    0;  Mismatches  246;  Indels   37;  Gaps   11;

Qy     15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74

Db     46 tctctgatggctgtcctgcagaaatctatgagtttttcccttatggggactttggccgcc 105

Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134

Db    106 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccgtcaacacc 165

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194

Db    166 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 225

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254

Db    226 ctggccaaggaggccagccttgcagataacaacacagacgtccggctcatcggggagaaa 285

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314

Db    286 ctgttccgaggagtcagtgctaaagatcagtgctacctgatgaagcaggtgctcaacttc 345

Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374

Db    346 accctggaagacgttctgctcccccagtcagacaggttccagccctacatgcaggaggtg 405

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434

Db    406 gtacctttcctgaccaaactcagcaatcagctcagctcctgtcacatcagcggtgacgac 465

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494

Db    466 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagt 525

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554

Db    526 ggagagatcaaggcgattggggaactggacctgctgtttatgtctctgagaaatgcttgc 585

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttttccctgctagaaataac 614
```

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Db    586 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 645

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
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Qy    675 catgatgggtggattccaaatgaaccccctgcgttagttacaaaggaaaccaatgccactt 734
          ||| ||  |  |||| || ||||| ||  ||     | | |||| |||      | |
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Qy    735 ttgtttataagaccagaaggtagacttttctaagcatagatatttattgataacatttcat 794
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Db    760 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 818

Qy    795 tgtaactggtgttctatacacagaaaacaatttatttttttaaataattgtctttttccat 854
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Db    819 tgtcactgatg----atacaacagaaaaataatgtactttaaaaaattgtttt-------g 867

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttcca 914
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Db    868 aaaggaggttacctctcattccttta---gaaaaaaagcttatgtaacttca--tttcca 922

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcatttttattta 974
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Db    923 tatccaatattttatatatgtaagtttatttattataagtata------cattttattta 976

Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
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Db    977 tgtcagtttattaatatggatttatttatagaaacattatctgctattgata-tttagta 1035

Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
          |||||| ||||   ||||||||||||||| ||| |    | |  |  | | || | | |
Db   1036 taaggcaaata---atatttatgacaataactatgg----aaacaagatatcttaggctt 1088

Qy   1095 caataaacacttggatatccta 1116
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Db   1089 taataaacacatggatatcata 1110


RESULT 15
AAD09746
ID   AAD09746 standard; cDNA; 778 BP.
XX
AC   AAD09746;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Mouse ZCYTO18 cDNA.
XX
KW   Mouse; cytostatic; cytokine; ZCYTO18 protein; genetic abnormality;
KW   cancer; inflammation; gene therapy; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             47..586
FT                   /*tag= a
FT                   /product= "Mouse ZCYTO18 protein"
FT   sig_peptide     47..145
FT                   /*tag= b
FT   mat_peptide     146..583
FT                   /*tag= c
FT                   /product= "Mouse mature ZCYTO18 protein"
XX
PN   WO200146422-A1.
XX
PD   28-JUN-2001.
XX
PF   22-DEC-2000; 2000WO-US35308.
XX
PR   23-DEC-1999;   99US-0471767.
PR   01-DEC-2000; 2000US-0250841.
XX
PA   (ZYMO ) ZYMOGENETICS INC.
XX
PI   Presnell SR,  Kindsvogel W;
XX
DR   WPI; 2001-408648/43.
DR   P-PSDB; AAE05052.
XX
PT   Novel human cytokine polypeptide, ZCYTO18, useful for treating cancer -
XX
PS   Example 5; Page 160-162; 167pp; English.
XX
CC   The patent discloses novel human cytokine, ZCYTO18 protein and its
CC   corresponding DNA. ZCYTO18 protein induces proliferation of cells
CC   expressing zcytor11, a receptor for ZCYTO18 or induces cytotoxicity
CC   in K5626 cells. ZCYTO18 DNA is useful for detecting a genetic
CC   abnormality in a patient. ZCYTO18 DNA and its antibodies are useful
CC   for detecting cancer and inflammation. ZCYTO18 protein is useful for
CC   killing cancer cells. It is useful for increasing platelets in a
CC   patient or injured tissue. It is also used in gene therapy.
CC   The present sequence is a cDNA encoding mouse cytokine, ZCYTO18.
XX
SQ   Sequence 778 BP; 213 A; 193 C; 197 G; 175 T; 0 other;


  Query Match             38.5%;  Score 429.2;  DB 22;  Length 778;
  Best Local Similarity   76.4%;  Pred. No. 5.6e-84;
  Matches  541;  Conservative    0;  Mismatches  163;  Indels    4;  Gaps    1;

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Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
          |||||||| |||||| | ||||| | ||  ||||  | |   ||   |||| ||| | ||
Db    101 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccgtcaacacc 160

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
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Db    161 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 220

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
          ||||| |||||||| ||| | || |||||||||||||| || || ||||| |||||||||
Db    221 ctggccaaggaggccagccttgcagataacaacacagatgtccggctcatcggggagaaa 280

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
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Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
          ||||| ||||| || ||| |||| || || || |||||||||||  || ||||||||||||
Db    341 accctggaagacgttctgctcccccagtcagacaggttccagccctacatgcaggaggtg 400

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
          ||||| |||||| |||  ||||||||   ||| ||| | ||||| ||    ||||| |||
Db    401 gtgcctttcctgaccaaactcagcaatcagctcagctcctgtcacatcagcggtgacgac 460

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
          | | | ||||||| ||||||   || |||||||||| |||||||||||||||||||||||||
Db    461 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagt 520

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
          |||||||||| || ||||| ||||||||  |||||||||||||||||||||||||||| |||
Db    521 ggagagatcaaggcgattggggaactggacctgctgtttatgtctctgagaaatgcttgc 580

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaaccccctttccctgctagaaataac 614
           | ||| |      |||||  |||| ||| ||||   ||    | ||| ||| ||| |||
Db    581 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 640

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
          ||| |||| ||  || |   ||||||     | |||||||  || ||||| ||  |||||
Db    641 aataagatccctgaatggacttttttt----actaaaggaaagtgagaagctaacgtccat 696

Qy    675 catgatgggtggattccaaatgaaccccctgcgttagttacaaaggaaa 722
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Db    697 catcattagaagatttcacatgaaacctggctcagttgaaaaagaaaa 744
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Job time: 4299 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:32:59 ; Search time 52.38 Seconds
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Perfect score: 1116
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	639	57.3	690	4	US-09-354-243B-24	Sequence 24, Appl
	2	525.2	47.1	1111	4	US-09-178-973B-9	Sequence 9, Appli
	3	525.2	47.1	1111	4	US-09-354-243B-9	Sequence 9, Appli
	4	524.4	47.0	1119	4	US-09-178-973B-7	Sequence 7, Appli
	5	524.4	47.0	1119	4	US-09-354-243B-7	Sequence 7, Appli
	6	216.4	19.4	5935	4	US-09-178-973B-17	Sequence 17, Appl
	7	216.4	19.4	5935	4	US-09-354-243B-29	Sequence 29, Appl
	8	215.6	19.3	7445	4	US-09-178-973B-8	Sequence 8, Appli
	9	215.6	19.3	7445	4	US-09-354-243B-8	Sequence 8, Appli
	10	207	18.5	4797	4	US-09-354-243B-25	Sequence 25, Appl
c	11	63.2	5.7	6243	2	US-09-056-075-1	Sequence 1, Appli
c	12	56.8	5.1	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	13	51.8	4.6	4254	2	US-08-443-639-7	Sequence 7, Appli
	14	51.8	4.6	8920	2	US-08-446-855A-1	Sequence 1, Appli
	15	51.8	4.6	8920	4	US-09-150-741-1	Sequence 1, Appli
c	16	50.2	4.5	767	4	US-08-998-416-472	Sequence 472, App
c	17	49	4.4	834	4	US-08-998-416-305	Sequence 305, App
c	18	47.6	4.3	1368	3	US-08-874-563-5	Sequence 5, Appli
c	19	47.6	4.3	1368	3	US-08-577-483-14	Sequence 14, Appl
	20	47.4	4.2	615	4	US-08-998-416-186	Sequence 186, App
	21	47.4	4.2	636	4	US-08-998-416-1137	Sequence 1137, Ap
c	22	47.4	4.2	701	4	US-08-998-416-701	Sequence 701, App
	23	47.4	4.2	837	4	US-08-998-416-288	Sequence 288, App
	24	46	4.1	782	4	US-09-007-119-15	Sequence 15, Appl
c	25	45.6	4.1	615	4	US-08-998-416-186	Sequence 186, App
c	26	45.6	4.1	636	4	US-08-998-416-1137	Sequence 1137, Ap
c	27	45.6	4.1	837	4	US-08-998-416-288	Sequence 288, App
	28	45.6	4.1	1214	4	US-08-817-913-13	Sequence 13, Appl
	29	45.6	4.1	1232	4	US-08-817-913-14	Sequence 14, Appl
	30	45.6	4.1	1352	4	US-08-817-913-15	Sequence 15, Appl
	31	45.6	4.1	1734	4	US-08-817-913-16	Sequence 16, Appl
	32	45.6	4.1	1920	4	US-08-817-913-17	Sequence 17, Appl
	33	45.4	4.1	1667	1	US-08-485-284A-1	Sequence 1, Appli
	34	45	4.0	676	4	US-08-998-416-1014	Sequence 1014, Ap
	35	45	4.0	677	4	US-08-998-416-920	Sequence 920, App
	36	44.8	4.0	658	4	US-08-998-416-193	Sequence 193, App
c	37	44.6	4.0	665	2	US-08-883-795A-36	Sequence 36, Appl
	38	44.6	4.0	26664	4	US-09-564-805-28	Sequence 28, Appl
c	39	44.6	4.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
c	40	44.6	4.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
c	41	44.6	4.0	246240	2	US-08-724-394A-22	Sequence 22, Appl
c	42	44.2	4.0	828	4	US-08-998-416-538	Sequence 538, App
c	43	44.2	4.0	6124	4	US-08-213-419B-3	Sequence 3, Appli
	44	44.2	4.0	19124	2	US-08-487-826B-13	Sequence 13, Appl
	45	44	3.9	3168	4	US-09-165-239A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-354-243B-24
; Sequence 24, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (TIFs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 24
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-354-243B-24

Query Match 57.3%; Score 639; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.4e-150;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
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Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Db    352 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 411

Qy    361 atatgcaggaggtggtgccccttcctggccaggctcagcaacaggctaagcacatgtcata 420

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Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480

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Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540

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Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600

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Qy    601 ctgctagaaataacaattagatgccccaaagcgattttt 639

Db    652 ctgctagaaataacaattagatgccccaaagcgattttt 690
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RESULT 2
US-09-178-973B-9
; Sequence 9, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
; TITLE OF INVENTION: (TIFs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543
; CURRENT APPLICATION NUMBER: US/09/178,973B
; CURRENT FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 9
; LENGTH: 1111
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-178-973B-9

Query Match 47.1%; Score 525.2; DB 4; Length 1111;
Best Local Similarity 73.8%; Pred. No. 8.8e-122;
Matches 813; Conservative 0; Mismatches 253; Indels 36; Gaps 10;

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Db     44 tcggtgatggctgtcctgcagaaatctatgagtttttcccttatggggactttggccgcc 103

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Qy    615 aattagatgccccaaagcgatttttttaaccaaaaggaagatgggaagccaaactccat 674

Db    644 aataagatccctgaatggacttttta----ctaaaggaaagtgagaagctaacgtccac 699

Qy    675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccactt 734

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Db    866 aaaggaggttacctctcattcctcta---gaagaaaagcctatgtaacttca--tttcca 920

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Qy   1095 caataaacacttggatatccta 1116

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RESULT 3
US-09-354-243B-9
; Sequence 9, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
; TITLE OF INVENTION: (TIFs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 9
; LENGTH: 1111

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;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
US-09-354-243B-9


  Query Match            47.1%;  Score 525.2;  DB 4;  Length 1111;
  Best Local Similarity  73.8%;  Pred. No. 8.8e-122;
  Matches  813;  Conservative    0;  Mismatches  253;  Indels   36;  Gaps   10;

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Qy      75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
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Db     104 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccatcaacacc 163

Qy     135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
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Db     164 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 223

Qy     195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
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Qy     255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
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Qy     315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
           ||||| |||||  | ||| |||| || || || ||||||| ||| || ||||||||||||
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Qy     375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
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Db     404 gtgcctttcctgaccaaactcagcaatcagctcagctcctgtcacatcagtggtgacgac 463

Qy     435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
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Qy     495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
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Qy     555 atttgaccagagcaaagctgaaaaatgaataactaacccccttttccctgctagaaataac 614
           | ||| |      |||||  |||| ||| ||||   ||    | ||| ||| ||| |||
Db     584 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 643

Qy     615 aattagatgccccaaagcgatttttttaaccaaaaggaagatgggaagccaaactccat 674
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Db     644 aataagatccctgaatggacttttta----ctaaaggaaagtgagaagctaacgtccac 699

Qy     675 catgatgggtggattccaaatgaaccccctgcgttagttacaaaggaaaccaatgccactt 734
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Qy     735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
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Db     758 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 816

Qy     795 tgtaactggtgttctatacacagaaaacaatttatttttttaaataattgtctttttccat 854
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Db     866 aaaggaggttacctctcattcctcta---gaagaaaagcctatgtaacttca--tttcca 920

Qy     915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
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Qy    1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
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Qy    1095 caataaacacttggatatccta 1116
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RESULT   4
US-09-178-973B-7
; Sequence 7, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 7
;   LENGTH: 1119
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-7


  Query Match            47.0%;  Score 524.4;  DB 4;  Length 1119;
  Best Local Similarity  74.3%;  Pred. No. 1.4e-121;
  Matches  819;  Conservative    0;  Mismatches  246;  Indels   37;  Gaps   11;

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Qy      75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
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Qy     255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
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Qy     315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
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Qy     435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
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Qy     495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
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Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
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Qy    675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccacttt 734
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Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
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Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
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Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
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Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
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RESULT 5
US-09-354-243B-7
; Sequence 7, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
; APPLICANT: Dumoutier, Laure
; APPLICANT: Louhed, Jamila
; APPLICANT: Renauld, Jean-Christophe
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
; TITLE OF INVENTION: (TIFs)
; TITLE OF INVENTION: The Proteins Encoded, and Uses Thereof
; FILE REFERENCE: LUD 5543.1
; CURRENT APPLICATION NUMBER: US/09/354,243B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US09/178,973
; PRIOR FILING DATE: 1998-10-26
; NUMBER OF SEQ ID NOS: 29
; SEQ ID NO 7
; LENGTH: 1119
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
US-09-354-243B-7

Query Match 47.0%; Score 524.4; DB 4; Length 1119;
Best Local Similarity 74.3%; Pred. No. 1.4e-121;
Matches 819; Conservative 0; Mismatches 246; Indels 37; Gaps 11;

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Qy     15 tctgcaatggccgccctgcagaaatctgtgagctctttccttatggggaccctggccacc 74
Db     46 tctctgatggctgtcctgcagaaatctatgagtttttcccttatggggactttggccgcc 105

Qy     75 agctgcctccttctcttggccctcttggtacagggaggagcagctgcgcccatcagctcc 134
Db    106 agctgcctgcttctcattgccctgtgggcccaggaggcaaatgcgctgcccgtcaacacc 165

Qy    135 cactgcaggcttgacaagtccaacttccagcagccctatatcaccaaccgcaccttcatg 194
Db    166 cggtgcaagcttgaggtgtccaacttccagcagccgtacatcgtcaaccgcacctttatg 225

Qy    195 ctggctaaggaggctagcttggctgataacaacacagacgttcgtctcattggggagaaa 254
Db    226 ctggccaaggaggccagccttgcagataacaacacagacgtccggctcatcggggagaaa 285

Qy    255 ctgttccacggagtcagtatgagtgagcgctgctatctgatgaagcaggtgctgaacttc 314
Db    286 ctgttccgaggagtcagtgctaaagatcagtgctacctgatgaagcaggtgctcaacttc 345

Qy    315 acccttgaagaagtgctgttccctcaatctgataggttccagccttatatgcaggaggtg 374
Db    346 accctggaagacgttctgctcccccagtcagacaggttccagccctacatgcaggaggtg 405

Qy    375 gtgcccttcctggccaggctcagcaacaggctaagcacatgtcatattgaaggtgatgac 434
Db    406 gtaccttttcctgaccaaactcagcaatcagctcagctcctgtcacatcagcggtgacgac 465

Qy    435 ctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagcttggagagagt 494
Db    466 cagaacatccagaagaatgtcagaaggctgaaggagacagtgaaaaagcttggagagagt 525

Qy    495 ggagagatcaaagcaattggagaactggatttgctgtttatgtctctgagaaatgcctgc 554
Db    526 ggagagatcaaggcgattggggaactggacctgctgtttatgtctctgagaaatgcttgc 585

Qy    555 atttgaccagagcaaagctgaaaaatgaataactaacccccttttccctgctagaaataac 614
Db    586 gtctgagcgagaagaagctagaaaacgaagaactgctccttcctgccttctaaaaagaac 645

Qy    615 aattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagccaaactccat 674
Db    646 aataagatccctgaatggacttttttta----ctaaaggaaagtgagaagctaacgtccat 701

Qy    675 catgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaccaatgccacttt 734
Db    702 catcattagaagatttcacatgaaacctggctcagttgaaaaagaaaatagtgtcaa--g 759

Qy    735 ttgtttataagaccagaaggtagactttctaagcatagatatttattgataacatttcat 794
Db    760 ttgtccatgagaccag-aggtagacttgataaccacaaagattcattgacaatattttat 818

Qy    795 tgtaactggtgttctatacacagaaaacaatttatttttaaataattgtctttttccat 854
Db    819 tgtcactgatg----atacaacagaaaaataatgtactttaaaaaattgttt-------g 867

Qy    855 aaaaaagattactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttcca 914
Db    868 aaaggaggttacctctcattcctttta---gaaaaaaagcttatgtaacttca--tttcca 922

Qy    915 taatcagtactttatatttataaatgtatttattattattataagactgcattttattta 974
Db    923 tatccaatattttatatatgtaagtttatttattataagtata------cattttattta 976

Qy    975 tatcattttattaatatggatttatttatagaaacatcattcgatattgctacttgagtg 1034
Db    977 tgtcagtttattaatatggatttatttatagaaacattatctgctattgata-tttagta 1035

Qy   1035 taaggctaatattgatatttatgacaataattatagagctataacatgtttatttgacct 1094
Db   1036 taaggcaaata---atatttatgacaataactatgg----aaacaagatatcttaggctt 1088

Qy   1095 caataaacacttggatatccta 1116
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Db   1089 taataaacacatggatatcata 1110


RESULT   6
US-09-178-973B-17
; Sequence 17, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
;   LENGTH: 5935
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-17


  Query Match             19.4%;  Score 216.4;  DB 4;  Length 5935;
  Best Local Similarity   69.9%;  Pred. No. 1.3e-44;
  Matches  446;  Conservative    0;  Mismatches  156;  Indels   36;  Gaps   10;

Qy     479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
           | |||||||||||||| |||||||||||||| || || ||||||||  |||||||||||| |
Db    5221 atagcttggagagagcggagagatcaaagcgatcggggaactggacctgctgtttatgtc 5280

Qy     539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttt 598.
           |||||||||||| ||| | ||| |      |||||  |||| ||| ||||   ||    |
Db    5281 tctgagaaatgcttgcgtctgagcgagaagaagctagaaaacgaagaactgctccttcct 5340

Qy     599 ccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatg 658
           ||| ||| ||| |||||| |||| ||  || |   ||||||     | |||||||  ||
Db    5341 gccttctaaaaagaacaataagatccctgaatggacttttttt----actaaaggaaagtg 5396

Qy     659 ggaagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaag 718
           |||||  ||  |||| ||| ||  |  |||| || ||||| ||  ||     | | | ||
Db    5397 agaagctaacgtccaccatcattagaagatttcacatgaaacctggctcagttgaaagag 5456

Qy     719 gaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatattt 778
           |||      | |   ||||  || ||||||| ||||||||||  ||| || | | |||
Db    5457 aaaatagtgtcaa--gttgtccatgagaccag-aggtagacttgataaccacaaagattc 5513

Qy     779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaat 838
           ||||| || |||| ||||| | || |     || ||    ||| | | | |  ||||||
Db    5514 attgacaatattttattgtcattgat----aatgcaacagaaaaagtatgtactttaaaa 5569

Qy     839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaacccctaaa 898
           |||||| |        |||  || |||| |  ||||||| ||   ||| |||  ||||
Db    5570 aattgttt-------gaaaggaggttacctctcattcctcta---gaagaaaagcctatg 5619

Qy     899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
           || |||||  |||||||||| || |||||||||| | ||| | |||||||||| | ||||
Db    5620 taacttca--tttccataaccaatactttatatatgtaagtttatttattataagtata- 5676

Qy     959 gactgcattttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
           |||||||||||| ||| ||||||||||||||||||||||||||| || ||  ||
Db    5677 -----cattttatttatgtcagtttattaatatggatttatttatagaaaaattatctga 5731

Qy    1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
           | ||| || |||||| ||| || ||||   ||||||||| ||||| |||||    | |
Db    5732 tgttgatatttgagtataaagcaaata---atatttatgataataactatag----aaac 5784

Qy    1079 catgtttatttgacctcaataaacacttggatatccta 1116
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Db    5785 aagatatcttaggctttaataaacacatgaatatcata 5822
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RESULT   7
US-09-354-243B-29
; Sequence 29, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 29
;   LENGTH: 5935
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-29


  Query Match             19.4%;  Score 216.4;  DB 4;  Length 5935;
  Best Local Similarity   69.9%;  Pred. No. 1.3e-44;
  Matches  446;  Conservative    0;  Mismatches  156;  Indels   36;  Gaps   10;

Qy     479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
           | |||||||||||||| |||||||||||||| || || ||||||||  |||||||||||| |
Db    5221 atagcttggagagagcggagagatcaaagcgatcggggaactggacctgctgtttatgtc 5280

Qy     539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttt 598
           |||||||||||| ||| | ||| |      |||||  |||| ||| ||||   ||    |
Db    5281 tctgagaaatgcttgcgtctgagcgagaagaagctagaaaacgaagaactgctccttcct 5340

Qy     599 ccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatg 658
           ||| ||| ||| |||||| |||| ||  || |   ||||||     | |||||||  ||
Db    5341 gccttctaaaaagaacaataagatccctgaatggacttttttt----actaaaggaaagtg 5396

Qy     659 ggaagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaag 718
           |||||  ||  |||| ||| ||  |  |||| || ||||| ||  ||     | | | ||
Db    5397 agaagctaacgtccaccatcattagaagatttcacatgaaacctggctcagttgaaagag 5456

Qy     719 gaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatattt 778
           |||      | |   ||||  || ||||||| ||||||||||  ||| || | | |||
Db    5457 aaaatagtgtcaa--gttgtccatgagaccag-aggtagacttgataaccacaaagattc 5513

Qy     779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaat 838
           ||||| || |||| ||||| | || |     || ||    ||| | | | |  ||||||
Db    5514 attgacaatattttattgtcattgat----aatgcaacagaaaaagtatgtactttaaaa 5569

Qy     839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaacccctaaa 898
           |||||| |        |||  || |||| |  ||||||| ||   ||| |||  ||||
Db    5570 aattgttt-------gaaaggaggttacctctcattcctcta---gaagaaaagcctatg 5619

Qy     899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
           || |||||  |||||||||| || |||||||||| | ||| | |||||||||| | ||||
Db    5620 taacttca--tttccataaccaatactttatatatgtaagtttatttattataagtata- 5676

Qy     959 gactgcattttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
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Db    5677 -----cattttatttatgtcagtttattaatatggatttatttatagaaaaattatctga 5731

Qy    1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
           | ||| || |||||| ||| || ||||   ||||||||| ||||| |||||    | |
Db    5732 tgttgatatttgagtataaagcaaata---atatttatgataataactatag----aaac 5784

Qy    1079 catgtttatttgacctcaataaacacttggatatccta 1116
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Db   5785 aagatatcttaggctttaataaacacatgaatatcata 5822


RESULT   8
US-09-178-973B-8
; Sequence 8, Application US/09178973B
; Patent No. 6274710
; GENERAL INFORMATION:
;  APPLICANT: Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION: Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fac
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE: LUD 5543
;  CURRENT APPLICATION NUMBER: US/09/178,973B
;  CURRENT FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 8
;   LENGTH: 7445
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-178-973B-8


  Query Match           19.3%;  Score 215.6;  DB 4;  Length 7445;
  Best Local Similarity  70.8%;  Pred. No. 2.3e-44;
  Matches  452;  Conservative    0;  Mismatches  149;  Indels   37;  Gaps   11;

Qy    479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
          | ||||||||||||||||||||||||| || ||||| ||||||||  ||||||||||||
Db   6535 atagcttggagagagtggagagatcaaggcgattggggaactggacctgctgtttatgtc 6594

Qy    539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttt 598
          |||||||||||| ||| | ||| |      |||||  |||| ||| ||||   ||    |
Db   6595 tctgagaaatgcttgcgtctgagcgagaagaagctagaaaacgaagaactgctccttcct 6654

Qy    599 ccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatg 658
           ||| ||| ||| |||||| |||| ||  || |   ||||||     | |||||||  ||
Db   6655 gccttctaaaaagaacaataagatccctgaatggacttttttt----actaaaggaaagtg 6710

Qy    659 ggaagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaag 718
          |||||  ||  |||||||| ||  |  |||| || ||||| ||  ||     | | ||||
Db   6711 agaagctaacgtccatcatcattagaagatttcacatgaaacctggctcagttgaaaaag 6770

Qy    719 gaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatattt 778
          |||      | |   ||||  || |||||||  ||||||||||  ||| || | | |||
Db   6771 aaaatagtgtcaa--gttgtccatgagaccag-aggtagacttgataaccacaaagattc 6827

Qy    779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaat 838
          ||||| || |||| ||||| |||| ||    |||||    ||| |   | |  ||||||
Db   6828 attgacaatattttattgtcactgatg----atacaacagaaaaataatgtactttaaaa 6883

Qy    839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaa 898
          ||||||  |        |||  || |||| |  ||||||||||   |||||||  | ||
Db   6884 aattgttt-------gaaaggaggttacctctcattccttta---gaaaaaaagcttatg 6933

Qy    899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
          || |||||  ||||||||  || || ||||||| | ||| | ||||||||| | ||||
Db   6934 taacttca--tttccatatccaatattttatatatgtaagtttatttattataagtata- 6990

Qy    959 gactgcattttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
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Db   6991 -----cattttatttatgtcagtttattaatatggatttatttatagaaacattatctgc 7045

Qy   1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
          ||||| || || ||| |||||| ||||   ||||||||||||||| ||| |    | |
Db   7046 tattgata-tttagtataaggcaaata---atatttatgacaataactatgg----aaac 7097

Qy   1079 catgtttatttgacctcaataaacacttggatatccta 1116
           |  | | || | | | |||||||| |||||||| ||
Db   7098 aagatatcttaggctttaataaacacatggatatcata 7135


RESULT   9
US-09-354-243B-8
; Sequence 8, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 8
;   LENGTH: 7445
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
US-09-354-243B-8


  Query Match           19.3%;  Score 215.6;  DB 4;  Length 7445;
  Best Local Similarity  70.8%;  Pred. No. 2.3e-44;
  Matches  452;  Conservative    0;  Mismatches  149;  Indels   37;  Gaps   11;

Qy    479 aaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtc 538
          | ||||||||||||||||||||||||| || ||||| ||||||||  ||||||||||||
Db   6535 atagcttggagagagtggagagatcaaggcgattggggaactggacctgctgtttatgtc 6594

Qy    539 tctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttt 598
          |||||||||||| ||| | ||| |      |||||  |||| ||| ||||   ||    |
Db   6595 tctgagaaatgcttgcgtctgagcgagaagaagctagaaaacgaagaactgctccttcct 6654

Qy    599 ccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatg 658
           ||| ||| ||| |||||| |||| ||  || |   ||||||     | |||||||  ||
Db   6655 gccttctaaaaagaacaataagatccctgaatggacttttttt----actaaaggaaagtg 6710

Qy    659 ggaagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaag 718
          |||||  ||  |||||||| ||  |  |||| || ||||| ||  ||     | | ||||
Db   6711 agaagctaacgtccatcatcattagaagatttcacatgaaacctggctcagttgaaaaag 6770

Qy    719 gaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatattt 778
          |||      | |   ||||  || |||||||  ||||||||||  ||| || | | |||
Db   6771 aaaatagtgtcaa--gttgtccatgagaccag-aggtagacttgataaccacaaagattc 6827

Qy    779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaat 838
          ||||| || |||| ||||| |||| ||    |||||    ||| |   | |  ||||||
Db   6828 attgacaatattttattgtcactgatg----atacaacagaaaaataatgtactttaaaa 6883

Qy    839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaa 898
          ||||||  |        |||  || |||| |  ||||||||||   |||||||  | ||
Db   6884 aattgttt-------gaaaggaggttacctctcattccttta---gaaaaaaagcttatg 6933

Qy    899 tagcttcatgtttccataatcagtactttatatttataaatgtatttattattattataa 958
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Db   6934 taacttca--tttccatatccaatattttatatatgtaagtttatttattataagtata- 6990

Qy    959 gactgcattttatttatatcattttattaatatggatttatttatagaaacatcattcga 1018
                |||||||||||| ||| ||||||||||||||||||||||||||||||||  ||  |
Db   6991 -----cattttatttatgtcagtttattaatatggatttatttatagaaacattatctgc 7045

Qy   1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
          ||||| || || ||| |||||| ||||   ||||||||||||||| ||| |    | |
Db   7046 tattgata-tttagtataaggcaaata---atatttatgacaataactatgg----aaac 7097

Qy   1079 catgtttatttgacctcaataaacacttggatatccta 1116
           |  | | || | | | |||||||| |||||||| ||
Db   7098 aagatatcttaggctttaataaacacatggatatcata 7135
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RESULT  10
US-09-354-243B-25
; Sequence 25, Application US/09354243B
; Patent No. 6359117
; GENERAL INFORMATION:
;  APPLICANT:  Dumoutier, Laure
;  APPLICANT:  Louhed, Jamila
;  APPLICANT:  Renauld, Jean-Christophe
;  TITLE OF INVENTION:  Isolated Nucleic Acid Molecules which Encode T Cell Inducible Fa
;  TITLE OF INVENTION:  (TIFs)
;  TITLE OF INVENTION:  The Proteins Encoded, and Uses Thereof
;  FILE REFERENCE:  LUD 5543.1
;  CURRENT APPLICATION NUMBER: US/09/354,243B
;  CURRENT FILING DATE:  1999-07-16
;  PRIOR APPLICATION NUMBER:  US09/178,973
;  PRIOR FILING DATE:  1998-10-26
;  NUMBER OF SEQ ID NOS:  29
; SEQ ID NO 25
;   LENGTH: 4797
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-354-243B-25


  Query Match             18.5%;  Score 207;  DB 4;  Length 4797;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-42;
  Matches  207;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 tcgagttagaattgtctgcaatggccgccctgcagaaatctgtgagctctttccttatgg 111

Qy      61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 171

Qy     121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     172 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 231

Qy     181 accgcaccttcatgctggctaaggagg 207
          |||||||||||||||||||||||||||
Db     232 accgcaccttcatgctggctaaggagg 258


RESULT  11
US-09-056-075-1/c
; Sequence 1, Application US/09056075
; Patent No. 5955368
;  GENERAL INFORMATION:
;    APPLICANT:  Johnson, Eric A.
;    APPLICANT:  Bradshaw, Marite
;    APPLICANT:  Rood, Julian
;    TITLE OF INVENTION:  Expression System for Clostridium
;    TITLE OF INVENTION:  Species
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53701-2113
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/056,075
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J.
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  960296.95238
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6243 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  3770..4013
;      OTHER INFORMATION:  /note= "RP4 origin of DNA transfer (oriT) from
;      OTHER INFORMATION:  plasmid RP4"
US-09-056-075-1


  Query Match             5.7%;  Score 63.2;  DB 2;  Length 6243;
  Best Local Similarity   48.9%;  Pred. No. 1.9e-06;
  Matches  170;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy     752 aggtagactttctaagcatagatatttattgataacatttcattgtaactggtgttctat 811
           | |||    |   ||   ||||   | ||       || | |    || |||  || |||
Db    1543 AAGTACCAATAAAAACATTAGAACGTCATATTACGTATATGAAAAAAAATGGGCTTTTAT 1484

Qy     812 acacagaaaacaatttatttttaaataattgtctttttccataaaaaagattactttcc 871
           | |    |    ||  || ||   |       || |   ||| |||| | |  ||| |
Db    1483 AAAGGCTCATTTTTTATATTCTTTTCTTCAAAGATTATATAATATAAAAAAATTTTTTTC 1424

Qy     872 attcctttaggggaaaaaacccctaaatagcttcatgtttccataatcagtactttatat 931
           |  | || |    |||| |    || ||   || || |||  ||  | |    ||| |||
Db    1423 AAACTTTAAATAAAAAATATTTTTATATTTTTTTATTTTTTTATTTTATATTTTTTTAT 1364

Qy     932 ttataaatgtatttattattattataagactgcattttatttatatcattttattaatat 991
           || |  || | | |||| || |  |    |      |||||||| |||  |||| |    | |
Db    1363 TTTTTTATTTTTATATTTTTTTATTTTTATATTTTTTTATTTTTATATTTTTTTATTTTT 1304

Qy     992 ggatttatttatagaaacatcattcgatattgctacttgagtgtaaggctaatattgata 1051
           ||||  |||||      ||  ||  || ||  || ||   | |      || | ||
Db    1303 ATATTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTTAT 1244

Qy    1052 tttatgacaataattatagagctataacatgtttatttgacctcaata 1099
           ||| | |   |  ||||     |||    |  || ||| |  |   ||
Db    1243 TTTTTTATTTTTTTTATTTTTTTATTTTTTTATTTTTTTATTTTTTTA 1196


RESULT  12
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
;  GENERAL INFORMATION:
;    APPLICANT:  Sim, Kim L.
;    APPLICANT:  Chitnis, Chetan
;    APPLICANT:  Miller, Louis H.
;    APPLICANT:  Peterson, David S.
;    APPLICANT:  Su, Xin-zhaun
;    APPLICANT:  Wellems, Thomas E.
;    TITLE OF INVENTION:  BINDING DOMAINS FROM PLASMODIUM VIVAX
;    TITLE OF INVENTION:  AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe Martens Olson & Bear
;      STREET:  620 Newport Center Drive  16th Floor
;      CITY:  Newport Beach
;      STATE:  California
;      COUNTRY:  US
```

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;      ZIP:  92660
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,826B
;      FILING DATE:  10-SEP-1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:  NIH121.001CP1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19124 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-487-826B-13


  Query Match             5.1%;  Score 56.8;  DB 2;  Length 19124;
  Best Local Similarity   48.7%;  Pred. No. 0.00011;
  Matches  154;  Conservative    0;  Mismatches  162;  Indels    0;  Gaps    0;

Qy    779 attgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaat 838
          |||  |   ||||  || ||  |  || | ||||     |    ||| ||||||||  |
Db  15773 ATTTTTTTAATTTTTTTTTATTTTATGATATATATTTTTATTTTAATATATTTTTTTCTT 15714

Qy    839 aattgtctttttccataaaaaagattactttccattcctttaggggaaaaaacccctaaa 898
            || | | |||  || | | | |||  |||   ||   |           |  ||
Db  15713 TTTTTTTTGTTTTTATGATATATATTTTTTTTTTTTTAATGTTTTTTTTTTTCTTCTTTT 15654

Qy    899 tagcttcatgtttccataatcagtactttatatttataaaatgtatttattattattataa 958
            ||  | |||  ||||||| |  ||| |   |  |||| | ||| | ||| || |
Db  15653 GTTTTTATTTTTTTTATAATCATTTTTTTTTTATATAAAATTTTTTTTTAATTTTTTTTT 15594

Qy    959 gactgcattttatttatatcattttattaatatggatttatttatagaaaacatcattcga 1018
            ||     ||||   | | | ||| ||| || ||  || | ||  || ||   | |||
Db  15593 GATAATCTTTTTCATTTTTTATTCTATCAAAATTTATATTTTATTATAATTTTTATTATT 15534

Qy   1019 tattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataa 1078
          | ||   |  |   | |     |  | ||  | ||| |     | | || |    | |
Db  15533 TTTTAAAAAATTTTTCTCCTTTTTTTTTTTTTTTTTTTTTTTATTTTAATAAATTTTTTTTT 15474

Qy   1079 catgtttatttgacct 1094
             || ||||  | |
Db  15473 ATATTTCATTTTTCTT 15458


RESULT  13
US-08-443-639-7/c
; Sequence 7, Application US/08443639
; Patent No. 5981843
;  GENERAL INFORMATION:
;    APPLICANT:  Chappell, Joseph
;    APPLICANT:  Yin, Shaohui
;    APPLICANT:  Cornett, Catherine A.G.
;    TITLE OF INVENTION:  Transcriptional Control Sequences and
;    TITLE OF INVENTION:  Methods
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:. Greenlee and Winner, P.C.
;      STREET:  5370 Manhattan Circle, Suite 201
;      CITY:  Boulder
;      STATE:  CO
;      COUNTRY:  US
;      ZIP:  80303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/443,639
;      FILING DATE:  18-MAY-1995
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ferber, Donna M.
;      REGISTRATION NUMBER:  33878
;      REFERENCE/DOCKET NUMBER:  69-94
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (303) 499-8080
;      TELEFAX:  (303) 499-8089
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4254 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Nicotiana tabacum
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(1217..1327, 1455..1718, 1806..2182,
;      LOCATION:  2259
;      LOCATION:  ..2477, 2609..2747, 2903..3148, 3262..3558)
US-08-443-639-7


  Query Match             4.6%;  Score 51.8;  DB 2;  Length 4254;
  Best Local Similarity   49.0%;  Pred. No. 0.0011;
  Matches  166;  Conservative    0;  Mismatches  172;  Indels    1;  Gaps    1;

Qy    690 ccaaatgaaccccctgcgttagttacaaaggaaaccaatgccacttttgtttataagacca 749
          | || ||     ||  |||   | || |  |||  ||    | ||||   ||||  |
Db    560 CAAAGTGTTATGCTTTGTTTTCTCCACACAAAAAAAAAATGAAATTTTAAATATATTAATT 501

Qy    750 gaaggtagactttctaagcatagatatttattgataacatttcattgtaactggtgttct 809
            | ||    |||  ||    | || | | ||| || |   |  | | |    | |||| |
Db    500 TCAAGTTAGTTTTTGAATTTAAAATTTCTTTTGGTATCGCTCTAGTTTTTATATTGTTTT 441

Qy    810 atacacagaaaacaatttatttttttaaataattgtctttttccataaaaaagattacttt 869
              ||| |      | |   | ||||     ||   |||||| | |||||| | |    |
Db    440 GATGACATAGGTATAATGTATCTTTACGCCTTTTATTTTTTCAAGAAAAAAAAGTTGCAT 381

Qy    870 ccattcctttaggggaaaaaaccccctaaatagcttcatgtttccataatcagtactttat 929
              |        | | | || |  | | |  | ||| | |  |||   |    | |||
Db    380 GGTCGCGCGCGCATGTACACACACACACACACATACATTTATATATATATATATATATAT 321

Qy    930 atttataaatgtatttattattattataagactgcattttatttatatcatttttattaat 989
          || |||| || ||| || |||   ||||    |  || ||| || ||| ||||| || |
Db    320 ATATATATATATATATA-TATATATATATATATATATATTTAATTCTATAATTTTCTTTAA 262

Qy    990 atggatttatttatagaaacatcattcgatattgctact 1028
            |       | || |||      |  | ||| |   || |
Db    261 CTTTTCACAATTTTAGTGTATTTTTCTGATTTATATAAT 223


RESULT  14
US-08-446-855A-1
; Sequence 1, Application US/08446855A
; Patent No. 5849573
;  GENERAL INFORMATION:
;    APPLICANT:  Stewart, Thomas S
```

```
;    APPLICANT:  Flores, Maria V
;    APPLICANT:  O'Sullivan, William J
;    TITLE OF INVENTION:  Nucleotide sequence encoding carbamoyl
;    TITLE OF INVENTION:  phosphate synthetase II
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon & Vanderhye PC
;      STREET:  1100 No. 5849573th Glebe Road, 8th Floor
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,855A
;      FILING DATE:  06-Jul-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mitchard, Leonard C
;      REGISTRATION NUMBER:  29.009
;      REFERENCE/DOCKET NUMBER:  47-80
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4000
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8920 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  genomic
US-08-446-855A-1


  Query Match             4.6%;  Score 51.8;  DB 2;  Length 8920;
  Best Local Similarity   53.1%;  Pred. No. 0.0015;
  Matches  110;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy     862 attactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttccataatcag 921
           ||||  || ||||||  | |    |  |||    ||||||  |  ||  |   |||
Db    8452 ATTAACTTTCATTCCATAACAACATCAAAAGTATAAATATATAAATAGTAATATATAATA 8511

Qy     922 tactttatatttataaatgtatttattattattataagactgcattttatttatatcatt 981
           ||   ||||| |||| || ||| |||   ||||     | |  ||| ||||||  |
Db    8512 TATAATATATATATATATATATATATATATATTTATTTATTTAATTATATTTACGTTTAA 8571

Qy     982 ttattaatatggatttatttatagaaacatcattcgatattgctacttgagtgtaaggct 1041
            ||||||||    ||| | |  |  |  ||||||   |  |  |  || | | |
Db    8572 ATATTAATAAATGTTTTTATTAAATATGATCATTAATTTATATTGATTTATTTTTTTATA 8631

Qy    1042 aatattgatatttatgacaataattat 1068
           ||| ||  |  |    ||||   ||||
Db    8632 AATTTTTGTTATATATACAAATTTTAT 8658


RESULT  15
US-09-150-741-1
; Sequence 1, Application US/09150741
; Patent No. 6183996
; GENERAL INFORMATION:
;  APPLICANT: Stewart et al.
;  TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
; Patent No. 6183996
;  TITLE OF INVENTION: Synthetase II
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/09/150,741
;  CURRENT FILING DATE: 1998-09-10
;  EARLIER APPLICATION NUMBER: PL6380
;  EARLIER FILING DATE: 1992-12-16
;  EARLIER APPLICATION NUMBER: AU93/00617
;  EARLIER FILING DATE: 1993-12-02
;  EARLIER APPLICATION NUMBER: 08/446,855
;  EARLIER FILING DATE: 1995-07-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 8920
;   TYPE: DNA
;   ORGANISM: Plasmodium falciparum
US-09-150-741-1


  Query Match             4.6%;  Score 51.8;  DB 4;  Length 8920;
  Best Local Similarity   53.1%;  Pred. No. 0.0015;
  Matches  110;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy     862 attactttccattcctttaggggaaaaaaccccctaaatagcttcatgtttccataatcag 921
           ||||  || ||||||  | |    |  |||    ||||||  |  ||  |   |||
Db    8452 attaactttcattccataacaacatgaaaagtataaatatataaatagtaatatataata 8511

Qy     922 tactttatatttataaatgtatttattattattataagactgcattttatttatatcatt 981
           ||   ||||| |||| || ||| |||   ||||     | |  ||| ||||||  |
Db    8512 tataatatatatatatatatatatatatatttatttatttaattatatttacgtttaa 8571

Qy     982 ttattaatatggatttatttatagaaacatcattcgatattgctacttgagtgtaaggct 1041
            ||||||||    ||| | |  |  |  ||||||   |  |  |  || | | |
Db    8572 atattaataaatgtttttattaaatatgatcattaatttatattgatttatttttttata 8631

Qy    1042 aatattgatatttatgacaataattat 1068
           ||| ||  |  |    ||||   ||||
Db    8632 aatttttgttatatatacaaattttat 8658


Search completed: September 23, 2002, 00:45:14
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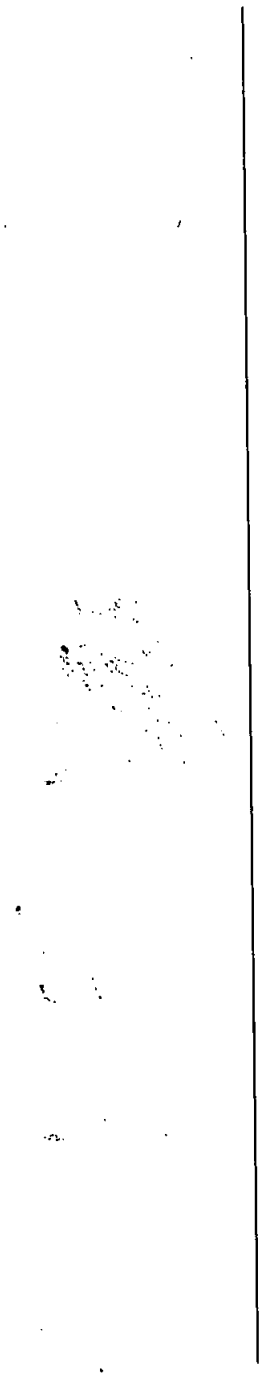

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 22, 2002, 23:30:13 ; Search time 1735.48 Seconds
(without alignments)
8679.214 Million cell updates/sec

Title: US-09-746-375-1
Perfect score: 1116
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttggatatccta 1116

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		257.8	23.1	700	11	AK005228	AK005228 Mus muscu
2		90	8.1	256	9	AV030414	AV030414 AV030414
3		82.6	7.4	1101	12	CNS00EVL	AL069706 Drosophil
4		77.2	6.9	1101	12	CNS0039G	AL063921 Drosophil
5		74.6	6.7	1043	12	CNS0145P	AL103735 Drosophil
c 6		73.2	6.6	1001	12	CNS0155H	AL105023 Drosophil
7		73.2	6.6	1101	12	CNS00BO1	AL057419 Drosophil
c 8		71.2	6.4	1101	12	CNS00EVL	AL069706 Drosophil
c 9		71	6.4	944	12	BH163008	BH163008 ENTTF3BTR
c 10		70.4	6.3	389	12	AQ104025	AQ104025 HS_3108_B
c 11		69.2	6.2	1092	12	CNS020K7	AL175696 Tetraodon
12		69	6.2	1225	12	CNS0161D	AL106171 Drosophil
13		68.6	6.1	1101	12	CNS000B8	AL063632 Drosophil
14		68.2	6.1	639	12	CNS038CX	AL232458 Tetraodon
c 15		68.2	6.1	996	12	CNS00FUH	AL071063 Drosophil
16		67.8	6.1	963	9	AL566565	AL566565 AL566565
17		67.8	6.1	1092	12	CNS020K7	AL175696 Tetraodon
18		67.6	6.1	832	12	CNS011OK	AL100526 Drosophil
c 19		67.6	6.1	928	12	CNS00DKY	AL071865 Drosophil
20		67	6.0	843	12	CNS00CS1	AL059666 Drosophil
c 21		67	6.0	1101	12	CNS017KE	AL108152 Drosophil
22		66.2	5.9	842	12	CNS00ACO	AL055007 Drosophil
c 23		66.2	5.9	895	12	CNS06FSV	AL396821 T7 end of
24		65.8	5.9	928	12	CNS00DKY	AL071865 Drosophil
c 25		65.8	5.9	1101	12	CNS00FYG	AL071206 Drosophil
26		65.8	5.9	1101	12	CNS016LI	AL106896 Drosophil
27		65.6	5.9	895	12	CNS06FSV	AL396821 T7 end of
c 28		65.2	5.8	905	12	CNS00KHX	AL077798 Drosophil
c 29		65	5.8	307	12	CNS00A3W	AL054893 Drosophil
30		64.8	5.8	912	12	AZ551630	AZ551630 ENTEM37TF
c 31		64.8	5.8	1200	12	CNS016CO	AL106578 Drosophil
32		64.6	5.8	1167	12	CNS07360	AL427102 clone BA0
33		64.4	5.8	851	12	BH149587	BH149587 ENTQB44TR
34		64.2	5.8	524	12	CNS01U9O	AL167541 Tetraodon
c 35		64.2	5.8	1190	12	CNS02ON7	AL206908 Tetraodon
36		64	5.7	987	12	CNS014PQ	AL104456 Drosophil
c 37		64	5.7	1101	12	CNS00EO7	AL069440 Drosophil
38		64	5.7	1101	12	CNS00FYG	AL071206 Drosophil
39		63.8	5.7	1101	12	CNS00CYH	AL060100 Drosophil
c 40		63.6	5.7	845	12	AQ745537	AQ745537 HS_2272_A
c 41		63.6	5.7	1137	12	CNS071NS	AL425150 clone BA0
42		63.4	5.7	874	12	AZ669565	AZ669565 ENTMN69TF
c 43		63.2	5.7	687	12	BH133925	BH133925 ENTNS77TR
c 44		63.2	5.7	879	12	BH164743	BH164743 ENTRG84TF
45		63.2	5.7	897	12	BH151924	BH151924 ENTPF95TF

ALIGNMENTS

RESULT 1
AK005228
LOCUS AK005228 700 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500012D04:interleukin 10-related T cell-derived inducible factor, full insert sequence.
ACCESSION AK005228
VERSION AK005228.1 GI:12837639
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male cerebellum cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1500012D04.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

```
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4  (sites)
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5  (bases 1 to 700)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence[5'
            GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCC 3']. cDNA
            was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3'
            end: SstI. Host: SOLR.
FEATURES             Location/Qualifiers
     source          1. .700
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="MGD:MGI:1900981"
                     /db_xref="taxon:10090"
                     /clone="1500012D04"
                     /sex="male"
                     /tissue_type="cerebellum"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="adult"
     gene            1. .700
                     /gene="Iltif"
     misc_feature    1. .700
                     /gene="Iltif"
                     /note="data source:MGD, source key:MGI:1355307,
                     evidence:ISS
                     interleukin 10-related T cell-derived inducible factor"
BASE COUNT      255 a    105 c    133 g    207 t
ORIGIN
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  Query Match           23.1%;  Score 257.8;  DB 11;  Length 700;
  Best Local Similarity   70.9%;  Pred. No. 5.7e-39;
  Matches  494;  Conservative    0;  Mismatches  167;  Indels   36;  Gaps   10;

Qy    417 catattgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtg 476
          || ||    ||||| |||| | | ||||||| ||||||   || |||||||| ||||||
Db     37 CACATCAGCGGTGACGACCAGAACATCCAGAAGAATGTCAGAAGGCTGAAGGAGACAGTG 96

Qy    477 aaaaagcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatg 536
          |||||||||||||||||| |||||||||||||| || || ||||||||  ||||||||||
Db     97 AAAAAGCTTGGAGAGAGCGGAGAGATCAAAGCGATCGGGGAACTGGACCTGCTGTTTATG 156

Qy    537 tctctgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccct 596
          ||||||||||||||| ||| | ||| |      |||||  |||| ||| ||||   ||
Db    157 TCTCTGAGAAATGCTTGCGTCTGAGCGAGAAGAAGCTAGAAAACGAAGAACTGCTCCTTC 216

Qy    597 ttccctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaaga 656
          | ||| ||| ||| |||||| |||| ||  || |   ||||||     | |||||||
Db    217 CTGCCTTCTAAAAAGAACAATAAGATCCCTGAATGGACTTTTTT----ACTAAAGGAAAG 272

Qy    657 tgggaagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaa 716
          || |||||  ||  |||| ||| ||  |  |||| || ||||| ||  ||     | | ||
Db    273 TGAGAAGCTAACGTCCACCATCATTAGAAGATTTCACATGAAACCTGGCTCAGTTGAAAA 332

Qy    717 aggaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatat 776
          || |||      | |   ||||  || |||||| ||||||||| ||| || | | ||
Db    333 AGAAAATAGTGTCAA--GTTGTCCATGAGACCAG-AGGTAGACTTGATAACCACAAAGAT 389

Qy    777 ttattgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttaa 836
          | ||||| || |||| ||||| |||| |     || ||    ||| | | | |  |||||
Db    390 TCATTGACAATATTTTATTGTCACTGAT----AATGCAACAGAAAAAGTATGTACTTTAA 445

Qy    837 ataattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccta 896
          | |||||| |        |||  || |||| |  |||||| |||  |||||    ||||
Db    446 AAAATTGTTT-------GAAAGGAGGTTACCTCTCATTCCTCTAGAAGAAAAG---CCTA 495

Qy    897 aatagcttcatgtttccataatcagtactttatatttataaatgtatttattattattat 956
            || |||||  ||||||||| || |||||||||| | ||| | |||||||||| | |||
Db    496 TGTAACTTCA--TTTCCATAACCAATACTTTATATATGTAAGTTTATTTATTATAAGTAT 553

Qy    957 aagactgcattttatttatatcattttattaatatggatttatttatagaaacatcattc 1016
          |     |||||||||||| ||| ||||||||||||||||||||||||||||| || ||
Db    554 A------CATTTTATTTATGTCAGTTTATTAATATGGATTTATTTATAGAAAAATTATCT 607

Qy   1017 gatattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctat 1076
          ||| ||| || |||||| ||| || ||||   |||||||||| ||||| |||||    |
Db    608 GATGTTGATATTTGAGTATAAAGCAAATA---ATATTTATGATAATAACTATAG----AA 660

Qy   1077 aacatgtttatttgacctcaataaacacttggatatc 1113
          |  |  | | || | | | |||||||||| || |||||
Db    661 ACAAGATATCTTAGGCTTTAATAAACACATGAATATC 697
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RESULT   2
AV030414
LOCUS       AV030414                 256 bp    mRNA    linear   EST 31-AUG-1999
DEFINITION  AV030414 Mus musculus adult C57BL/6J cerebellum Mus musculus cDNA
            clone 1500012D04, mRNA sequence.
ACCESSION   AV030414
VERSION     AV030414.1  GI:4829962
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 256)
  AUTHORS   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,
            Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara
            ,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J.,
            Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Owa,C.,
            Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara
            ,Y., Suzuki,H., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N.,
            Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Yoshino,M.,
            Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chie Owa
            Genome Science Laboratory
            RIKEN
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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            Tel: 81-298-36-9145
            Fax: 81-298-36-9098
            Email: genome-res@rtc.riken.go.jp
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length cDNA
            (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES              Location/Qualifiers
     source           1. .256
                      /organism="Mus musculus"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="1500012D04"
                      /clone_lib="Mus musculus adult C57BL/6J cerebellum"
                      /sex="male"
                      /tissue_type="cerebellum"
                      /dev_stage="adult"
BASE COUNT       88 a     29 c     41 g     98 t
ORIGIN


  Query Match             8.1%;  Score 90;  DB 9;  Length 256;
  Best Local Similarity   72.1%;  Pred. No. 3e-07;
  Matches  147;  Conservative    0;  Mismatches   50;  Indels    7;  Gaps    2;

Qy     910 ttccataatcagtactttatatttataaatgtatttattattattataagactgcatttt 969
           || | |   ||  ||      |||||| ||||   | |  ||||||||||  | ||||||
Db      60 TTTCCTTTCCATAACCGATACTTTATATATGTGAGTTTATTTATTATAAGTATACATTTT 119

Qy     970 atttatatcattttattaatatggatttatttatagaaacatcattcgatattgctactt 1029
           |||||| ||| ||||||||||||||||||||||||||||| || ||  ||| ||| || ||
Db     120 ATTTATGTCAGTTTATTAATATGGATTTATTTATAGAAAAATTATCTGATGTTGATATTT 179

Qy    1030 gagtgtaaggctaatattgatatttatgacaataattatagagctataacatgtttattt 1089
           |||| ||| || ||||   |||||||||| ||||| |||||    | |  |  | | ||
Db     180 GAGTATAAAGCAAATA---ATATTTATGATAATAACTATAG----AAACAAGATATCTTA 232

Qy    1090 gacctcaataaacacttggatatc 1113
           | | | |||||||||| || |||||
Db     233 GGCTTTAATAAACACATGAATATC 256


RESULT   3
CNS00EVL
LOCUS       CNS00EVL                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069706
VERSION     AL069706.1  GI:4949849
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES              Location/Qualifiers
     source           1. .1101
                      /organism="Drosophila melanogaster"
                      /db_xref="taxon:7227"
                      /clone_lib="RPCI-98"
                      /clone="BACR29B23"
                      /note="end : T7"
BASE COUNT      419 a     91 c     60 g    299 t    232 others
ORIGIN


  Query Match             7.4%;  Score 82.6;  DB 12;  Length 1101;
  Best Local Similarity   35.7%;  Pred. No. 7.7e-06;
  Matches  139;  Conservative   78;  Mismatches  172;  Indels    0;  Gaps    0;

Qy     713 acaaaggaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatag 772
           | |||  |:|  ||:   : | :    : ||| |  | ||  :| :  |: ::|  |||
Db     698 AAAAAAAAWATWAAWAATWATAWATAAWTTAAAAWAATAAAAWAAWAATWAWWATAATAT 757

Qy     773 atatttattgataacatttcattgtaactggtgttctatacacagaaaacaatttatttt 832
           ::|| |||   |:  :::  ::  ::  |    :    : | | |:|  ||| :|| :
Db     758 WWATATATAWTTWTAWWWATWWAWWWTATAWATAWAATAWAAWAWAWATAAATAWATAWA 817

Qy     833 ttaaataattgtctttttccataaaaaagattactttccattcctttaggggaaaaaacc 892
           |:|||:|: : | :: |:  |||::||  : :|      :|    |:|     ||:||
Db     818 TWAAAWAWAWATAWWATWATATAWWAATAWAWAAAAAATWTAATATWAATWATAAWAAAA 877

Qy     893 cctaaatagcttcatgtttccataatcagtactttatatttataaatgtatttattatta 952
           ||:|:   :|  | |::  :  || | :|  | : | : | |||   |      : ::
Db     878 AATAWAWTTWWTWTTTTWWAWWATATAAAWAWATAWAAAWAAAAAAAAAAAAAATAAWAWW 937

Qy     953 ttataagactgcattttatttatatcattttattaatatggatttatttatagaaacatc 1012
           :|:  |   |   |   :|:|||::  |: | ::|:|:|:|  |:||:| |:|| | | ::
Db     938 WTWATATTWTTATTAAAWTWTATWWATTWATTWWAWTWTATAWTTWTATWTATATATWWT 997

Qy    1013 attcgatattgctacttgagtgtaaggctaatattgatatttatgacaataattatagag 1072
           |:|  ||||   || |  : | ||     :| |:| |||| |:  | ::||: |||| |
Db     998 AWTAWATATATTTATTAAWWTATATTTTAWAAAWTAATATATWATAWWWTAWATATAWAW 1057

Qy    1073 ctataacatgtttatttgacctcaataaa 1101
           || |  | | |||:| |  | :: |||
Db    1058 WAATTAWTTATATATWTAAWATAWWAAAA 1086


RESULT   4
CNS0039G
LOCUS       CNS0039G                1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC #
            BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL063921
VERSION     AL063921.1  GI:4941778
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
```

```
          The BDGP is constructing a physical map of the Drosophila
          melanogaster genome using these BACs. For further information
          please see  http://www.fruitfly.org The BDGP Drosophila
          melanogaster BAC library was prepared by Kazutoyo Osoegawa and
          Aaron Mammoser in Pieter de Jong's laboratory in the Department of
          Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
          NY. The library is named RPCI-98 and was constructed by partial
          EcoRI digestion of Drosophila DNA provided by the BDGP from the
          isogenic strain y2; cn bw sp, the same strain used for the BDGP's
          P1 and EST libraries. A more detailed description of the library
          and how to order individual BAC clones, the entire library, or
          filters for hybridization from the BACPAC Resource Center can be
          found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR08K10"
                     /note="end : TET3"
BASE COUNT      201 a     64 c    131 g    202 t    503 others
ORIGIN


  Query Match             6.9%;  Score 77.2;  DB 12;  Length 1101;
  Best Local Similarity   18.7%;  Pred. No. 8.1e-05;
  Matches  128;  Conservative  274;  Mismatches  280;  Indels    2;  Gaps    1;

Qy    424 aaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaaagc 483
          :||| :: |    | :     :|:::::  :      ::  ::|||  : :: :::::::
Db    296 RAGGRRRRGGNGNGARGGRRRRGRRRRRRRAAAGGGRRRRRRAGGGGRARRRRRRRRRR 355

Qy    484 ttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctctga 543
          ||:||: | ||:: ||    :| :   || :    ||: |   : ::::: | | |
Db    356 RGGGRGARGGAGGRRGGAGGGGRGGRGGGGGGRGGGGGGMATATAWAWWWWWTTTTTTTT 415

Qy    544 gaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaacccccttccctg 603
          :||       | || :  : :  |||  | :||||: || :| ||:     :|:
Db    416 AWAAAWAAAATAATTWWAAWAWAAAAAATTWWAAAAWAAAAWAWTAWWTTTAWTWAAAAA 475

Qy    604 ctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaag 663
          | |||| :   ||  :|      :|   :||:::|| ||  ||||  || |:   :|
Db    476 AAAAAAATTWTTTTTTTWTTTAWTTWATAWWTTWWWTTAAAWAAAAAAAAAAAWAAAWAA 535

Qy    664 ccaaactccatcatgatgggtggattccaaatgaaccccTgcgttagttacaaaggaaac 723
          | |    :  : | : : |  |:   |:::: :   |:: :|       :: :
Db    536 AWATAAATWTWWTWWTTYTTWAAWATAAAMCMAAWYYHTYTTYTYHYYTYWTYTMTWHYH 595

Qy    724 caatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttattga 783
          : |   |:||:: ::: :|: : :  ::  :| :::|||:||| : :     :::  : :
Db    596 TMYTHAWAHTTWYHWYHTYAMWHWMTWHWTMWAWWHWTTYTAAYYYYYTCMYYYHYMHWH 655

Qy    784 taacatttcattgtaactggtgttctatacacagaaaacaatttatttttaaataattg 843
          :|: :    :|| |:: :  :  |:: : :::  :: :| :| : :::::::   ::|:
Db    656 HAHAHAAAWWTTHTWWTHAYHWATYHYYYYMYCAMMCMCTHTCHHCYYYYHHYTAHHTHT 715

Qy    844 tctttttccataaaaaagattactttccattcctttaggggaaaaaaccccTaaat--ag 901
          :::: :::::: ::|   ::    |:::::::::::|    : |:|: : ::::|:  |
Db    716 HHWYAHYYMWYYMWAYYWMYCTACTYHYHHHHHYHWAYHTTWYAWAHAMWMWHHAHYAAA 775

Qy    902 cttcatgtttccataatcagtactttatatttataaatgtatttattattattataagac 961
          : |: ||:::::  ::: : : ::|  ::  :  :::::|  | :|: ::: :
Db    776 AAWAAWATTHHYHHTTHYMHHTYMYHYYMYTCCYMCTYHCWHYYHTAYTCWTWTHHWMWT 835

Qy    962 tgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgatat 1021
          : :::::|:::: | : |:::|:|: ::::   |:|: |: :| : :::::: :: :::
Db    836 WTHWYHHTWWHHTTTHWAWWHTHTWCWWWWHATTWTWATHCWACMTMHWHHWMHMHHHHM 895

Qy   1022 tgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataacat 1081
          : :::| :   :::  || ::::|  ::| ::  :::::::::: | :  |:| :::
Db    896 ACHAHHHTHMCMCHHHMHCTCHHHHTMYHMTCHWMWHMHWHWHHWWMATWMTTMTTMMMM 955

Qy   1082 gtttatttgacctcaataaacact 1105
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             :::  ::: :::::  |:::
Db    956 CCMMHHHCHMYHMMHMYMYCCHYY 979


RESULT   5
CNS0145P
LOCUS       CNS0145P                1043 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN11G11 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL103735
VERSION     AL103735.1  GI:5615346
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1043)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1043
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN11G11"
                     /note="end : T7"
BASE COUNT      277 a     96 c    121 g    382 t    167 others
ORIGIN


  Query Match             6.7%;  Score 74.6;  DB 12;  Length 1043;
  Best Local Similarity   39.2%;  Pred. No. 0.00025;
  Matches  136;  Conservative   54;  Mismatches  157;  Indels    0;  Gaps    0;

Qy    760 tttctaagcatagatatttattgataacatttcattgtaactggtgttctatacacagaa 819
          ||| ||   |:| |:::| |:|  |||| | | :  | ||  |  |  | |||: | : |
Db    554 TTTWTATATAWATAWWTATWTATATAAAAATAMTATATATATTTTTATATATWAAAWAAT 613

Qy    820 aacaatttatttttaaataattgtctttttccataaaaaagattactttccattccttt 879
          |   || |:|||||| ::: :|: |  |:|:  | | | |   ||  |:|  :||  |:|
Db    614 ATWTATATWTTTTTTTWWWTWTWTTTATWTWWWAAATATATWTTTTWTWTWTWTTTTTWT 673

Qy    880 aggggaaaaaaccccTaaatagcttcatgtttccataatcagtactttatatttataaat 939
          :      | ::    |:|  |   |  | | |  ||| | |    | |:| |: ||  ||
Db    674 WTATATTATWWTWTWTWATAAATATTTTTTATWTATATTTATATWTATWTTTWAATTTAT 733

Qy    940 gtatttattattattataagactgcattttatttatatcattttattaatatggatttat 999
          |||||:  ||  || |     |   |||| ||| | |  ||||   || |:  | ::::
Db    734 ATATTTWANATANTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAAAAWAAAAWWWW 793

Qy   1000 ttatagaaacatcattcgatattgctacttgagtgtaaggctaatattgatatttatgac 1059
          ::::: |:: :: ::   |:| |  |  || : | :      :||||  ::|: ||: :
Db    794 WWWWWAAWWWWWWWWAWAAWAATTTTTTTTTTHHTTYCCYYTAWATATATWWAWATAWAWA 853

Qy   1060 aataattatagagctataacatgtttatttgacctcaataaacactt 1106
          :| ||  | | |   | || |      |    ||  |:|:|: |
Db    854 WAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAMAHAYAT 900
```

```
RESULT   6
CNS0155H/c
LOCUS       CNS0155H               1001 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN13C23 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL105023
VERSION     AL105023.1  GI:5617037
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1001)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1001
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN13C23"
                     /note="end : SP6"
BASE COUNT      266 a    219 c    134 g    150 t    232 others
ORIGIN

  Query Match             6.6%;  Score 73.2;  DB 12;  Length 1001;
  Best Local Similarity   40.9%;  Pred. No. 0.00046;
  Matches  108;  Conservative   50;  Mismatches  106;  Indels    0;  Gaps    0;

Qy     826 ttatttttttaaataattgtctttttccataaaaaagattactttccattcctttagggga 885
           |: ::||:|:| |  || | ||| |   ||:|  | :| : :||   |:  :: :    |
Db     982 TWTWWTTWTWATTTTTTATWTTTATTWTTAWATTAAWTAWAWTTATTTWTTWWAWAAWAA 923

Qy     886 aaaaaccccctaaatagcttcatgtttccataatcagtactttatatttataaatgtattt 945
           |:|::    ||:::|  ||  :  ||  ||: |   |  ||| |:|||   | : :|||:
Db     922 AWAWHTWTWTAWWWAAWTTTTWAATTTTATWTTWTTTTTTTTTTHTTTTATATWTWATTW 863

Qy     946 attattattataagactgcattttatttatatcattttattaatatggatttatttatag 1005
           :||:|: ||| || | |  ||||| |||::   :||||:: | | |  |||| |:|:|:
Db     862 WTTWTWTTTAAAAAATTWAATTTTTTTTTWWTAWWTTTTWWAATTTTTWATTTTTWTWTWT 803

Qy    1006 aaacatcattcgatattgctacttgagtgtaaggctaatattgatatttatgacaataat 1065
           ||| ||  ||  |:||  |   |       :|   |  |||| ::::||:| :    ::|
Db     802 AAATATTTTTTTAWWTTTTTTTATTTWATAWAAHTTTTTATTTWWWWTTWTWWWTTAWWT 743

Qy    1066 tatagagctataacatgtttattt 1089
            ||     | |:   | ::|  ||
Db     742 AATTTTTTTYTHYTYTTWYTTATT 719


RESULT   7
CNS00BO1
LOCUS       CNS00BO1               1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR24D09 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL057419
VERSION     AL057419.1  GI:4937885
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR24D09"
                     /note="end : T7"
BASE COUNT      420 a     56 c     48 g    261 t    316 others
ORIGIN

  Query Match             6.6%;  Score 73.2;  DB 12;  Length 1101;
  Best Local Similarity   43.6%;  Pred. No. 0.00046;
  Matches  169;  Conservative   50;  Mismatches  162;  Indels    7;  Gaps    2;

Qy     715 aaaggaaaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagat 774
           |||  |||:    :  | ||:| |:|:|  :   | ||  || ::   :|  :  |  |
Db     623 AAAATAAAYASCASAAAATTWTMTWTWTTTSTAAAAAATATAAWBSSVSTGBSATTKTAS 682

Qy     775 atttattgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttt 834
           |:|||||  :|:|:|||  :  |:::: :::   | ||||  | |  |||| |||||:|||||
Db     683 AWTTATTTWTWABATTGSSSTKBMWAKBS---TTTATAAAAAAAAAAAAATTTWTTTTTA 739

Qy     835 aaataattgtctttttccataaaaaagattactttccattcctttaggggaaaaaacccc 894
           : |  || | |||||  :: : |   |||  | |  |||  :|:|    |||:||
Db     740 TWTTTTTTTTTTTTTTWTWWTWTATTAATTTATATAAATTAAWTWAAAAAAAAWAAAAAT 799

Qy     895 taaatagcttcatgtttccataatcagtactttatatttataaatgt----atttattat 950
           :|  :|     :  |    | ||  |  | |  | : | ||:|:| |    |||||  |:
Db     800 WATTWAAAAAAWAATAAAAAAAAAAAAAAAATAAAAWATAATWAWTWTATAAATTTAATWA 859

Qy     951 tattataagactgcattttatttatatcattttattaatatggatttatttatagaaaca 1010
            || |||| : :  ||   |:  |  | |||| | :|||||  |  || ||:|  | |
Db     860 AATAATAAAWAWAAATAAAAWAAAATTTATTTAAAWAATATTAAAATAATTWTTTATATT 919

Qy    1011 tcattcgatattgctacttgagtgtaaggctaatattgatatttatgacaataattatag 1070
           |  ||   :| |  :| || |   ||    | | ||| | :   || : || | |:| |
Db     920 TTTTTTATWAATTTWAATTAAAAATATAAATTAAATTAAAWAAAATWWAAAAATTWAAAA 979

Qy    1071 agctataacatgtttatttgacctcaat 1098
           |  | |||  |  ||:| || |  : |:|
Db     980 AWATTTAAAAATTTWAATTAAAAWAAWT 1007


RESULT   8
CNS00EVL/c
```

```
LOCUS       CNS00EVL                1101 bp    DNA     linear   GSS 04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC:
            BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL069706
VERSION     AL069706.1  GI:4949849
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR29B23"
                     /note="end : T7"
BASE COUNT      419 a     91 c     60 g    299 t    232 others
ORIGIN
```

```
  Query Match             6.4%;  Score 71.2;  DB 12;  Length 1101;
  Best Local Similarity   35.8%;  Pred. No. 0.0011;
  Matches  118;  Conservative   67;  Mismatches  145;  Indels    0;  Gaps    0;

Qy     760 tttctaagcatagatatttattgataacatttcattgtaactggtgttctatacacagaa 819
           ||| : |   || |||| || : |    :|:|   | ||: : |  | |||  :   :
Db    1085 TTTWWTATWTTAWATATATAAWTAATTWWTWTATATWTAWWWTATWATATATTAWTTTWT 1026

Qy     820 aacaatttatttttttaaataattgtctttttccataaaaaagattactttccattccttt 879
           || |  | ::||  ||||||  | | :| ::  ||| |:|  :  :  |   :|:   |:
Db    1025 AAAATATAWWTTAATAAATATATWTAWTAWWATATATAWATAWAAWTATAWAWTWWAATW 966

Qy     880 aggggaaaaaacccctaaatagcttcatgtttccataatcagtactttatatttataaaat 939
           |     | |:|:      ||:|   | |: :|:  ||  |   |  |||:| |:|||: :|
Db     965 AATWWATAWAWTTTAATAAWAATATWAWWWTWTTATTTTTTTTTTTTTTWTTTWTATWTWT 906

Qy     940 gtatttattattattataagactgcattttatttatatcattttattaatatggatttat 999
           ||| |::|:: |  : :: | |  ||||| |:|  :  |: |||||:  |   |:|:|
Db     905 TTATATWWTWWAAAAWAWWAAWTWTATTTTTTWTTATWATTWATATTAWATTTTTTWTWR 846

Qy    1000 ttatagaaacatcattcgatattgctacttgagtgtaaggctaatattgatatttatgac 1059
           | :: | | :  ::|  :|:|:  |: |: | :       : :|:||    |:|||
Db     845 ATTWWTATATWATWWTATWTWTWTTTWATWTATWTATTTATWTWTWTTWTATTWTATWTA 786

Qy    1060 aataattatagagctataacatgtttattt 1089
           |:::|::   :   : |: || | |:: |
Db     785 TAWWWTWWATWWWTAWAAWTATATATWWAT 756
```

```
RESULT   9
BH163008/c
LOCUS       BH163008                944 bp    DNA     linear   GSS 24-SEP-2001
DEFINITION  ENTTF38TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
            genomic, DNA sequence.
ACCESSION   BH163008
VERSION     BH163008.1  GI:15736446
KEYWORDS    GSS.
SOURCE      Entamoeba histolytica.
  ORGANISM  Entamoeba histolytica
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1  (bases 1 to 944)
  AUTHORS   Loftus,B., Wang,Z., Van Aken,S. and Fraser,C.
  TITLE     Determination of clone end sequences from Entamoeba histolytica
            HM1:IMSS sheared DNA library (2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
            DNA library
            Seq primer: M13-Reverse
            Class: shotgun
            High quality sequence start: 13
            High quality sequence stop: 559.
FEATURES             Location/Qualifiers
     source          1. .944
                     /organism="Entamoeba histolytica"
                     /strain="HM1:IMSS"
                     /db_xref="taxon:5759"
                     /clone_lib="Entamoeba histolytica Sheared DNA"
                     /note="Vector: pHOS1; Site_1: Bst I; Constructed at The
                     Institute for Genomic Research (TIGR), Rockville, MD.
                     Genomic DNA isolated from broth cultures of E. histolytica
                     using a  method described by Clark and Diamond (Clark,
                     C.G., and Diamond, L.S.  (1993) Entamoeba histolytica: a
                     method for isolate identification.  Exp. Parasitol.
                     77:450.). The DNA was mechanically sheared to give a
                     tight size distribution (~2 kb). The v + 1 method used for
                     the library  construction is described in detail in Smith,
                     H.O. and Venter, J.C.  (Making small insert libraries for
                     whole genome shotgun sequencing  projects. In Genome
                     Sequencing: A Practical Approach, eds. M. Vaudin  and B.
                     Barell, Oxford University Press, 1999)."
BASE COUNT      430 a     67 c    197 g    250 t
ORIGIN
```

```
  Query Match             6.4%;  Score 71;  DB 12;  Length 944;
  Best Local Similarity   50.4%;  Pred. No. 0.0012;
  Matches  173;  Conservative    0;  Mismatches  170;  Indels    0;  Gaps    0;

Qy     773 atatttattgataacatttcattgtaactggtgttctatacacagaaaacaatttatttt 832
           ||| |||||      ||  | || || ||     | | ||      | |  |||||
Db     594 ATACTTATTATCTCTATACCTTTATACCTTTATATGTTTATCTCTTCATCTCTTTATACC 535

Qy     833 ttaaataattgtctttttccataaaaaagattactttccattcctttaggggaaaaaacc 892
           ||||||| || | | | |  ||| | |   |      |  || ||||||       | |
Db     534 TTAAATACTTCTATATATGTATATATATTTTATACCTTTATACCTTTATACCTTTATATG 475

Qy     893 cctaaatagcttcatgtttccataatcagtactttatatttataaatgtatttattatta 952
             ||  |  |||||| ||  | |    |||||| | || |||| | |||  |||
Db     474 TTTATATGTTTATATGTTTATATGTTTATATGTTTATATGTTTATATGTTTATATCTTTA 415

Qy     953 ttataagactgcattttatttatatcattttattaatatggatttatttatagaaacatc 1012
           |      |     || ||| | |||   |||||  | |  || | | |||    | |||
Db     414 TATGTTTATATGTTTATATCTTTATATCTTTATATCTTTATATCTTTATATCTTTATATC 355

Qy    1013 attcgatattgctacttgagtgtaaggctaatattgatatttatgacaataattatagag 1072
```

```
Db    354 TTTATACCTTTATATTATCTACTTCTATATATATTCCTATTTATATTCCTATTCTTCCCC 295

Qy   1073 ctataacatgtttatttgacctcaataaacacttggatatcct 1115
Db    294 CTTTTATATACTTATTATTTCCTTATATACACCCTTATATACT 252


RESULT 10
AQ104025/c
LOCUS       AQ104025                389 bp    DNA     linear   GSS 28-AUG-1998
DEFINITION  HS_3108_B1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3108 Col=1 Row=F, DNA sequence.
ACCESSION   AQ104025
VERSION     AQ104025.1  GI:3478961
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 389)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 3108  row: F  column: 1
            Class: BAC ends
            High quality sequence stop: 389.
FEATURES             Location/Qualifiers
     source          1. .389
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=3108 Col=1 Row=F"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT      119 a     86 c     65 g    118 t      1 others
ORIGIN


  Query Match             6.3%;  Score 70.4;  DB 12;  Length 389;
  Best Local Similarity   92.5%;  Pred. No. 0.0015;
  Matches   74;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy    413 atgtcatattgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacac 472
Db    148 ATAGCATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACAC 89

Qy    473 agtgaaaaagcttggagaga 492
Db     88 AGTGAAAAAGGTAGGACTGA 69


RESULT 11
CNS020K7/c
LOCUS       CNS020K7                1092 bp    DNA     linear   GSS 12-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            222L11 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL175696
VERSION     AL175696.1  GI:7813753
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1092)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1092)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1092)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1092
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="222L11"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG222CF06LP1~end : T7"
BASE COUNT      383 a    169 c    165 g    262 t    113 others
ORIGIN


  Query Match             6.2%;  Score 69.2;  DB 12;  Length 1092;
  Best Local Similarity   39.0%;  Pred. No. 0.0026;
  Matches  134;  Conservative   50;  Mismatches  160;  Indels    0;  Gaps    0;

Qy    760 tttctaagcatagatatttattgataacatttcattgtaactggtgttctatacacagaa 819
Db   1036 TTAATATATAAATATTTTATTTWTTTATATTTTATTTTTTTTTTTTTTTTAAAAATAAATT 977

Qy    820 aacaatttatttttttaaataattgtctttttccataaaaaagattactttccattccttt 879
Db    976 AAWWTTTTNWTTTATATTTTTTTTTTTTTWTTAWAAAAAWWAAAAAAAAAAAAAWATTTA 917

Qy    880 aggggaaaaaaccccctaaatagcttcatgtttccataatcagtactttatatttataaaat 939
Db    916 WAWWTWAWAAAAAAAAWWAWTTWTTTTTTAATTTTTTTTTTTTAWATTWWAATTTWTAAAW 857

Qy    940 gtatttattattattataagactgcattttatttatatcattttattaatatggatttat 999
Db    856 TWTTTTAAAWAATTATTTWWTTTTTTAWTAAWTAAAWTNTTTTWTTTAAAATAWAAWWTW 797

Qy   1000 ttatagaaacatcattcgatattgctacttgagtgtaaggctaatattgatatttatgac 1059
Db    796 ATWWWTAAAAWTAAWAWWWTTTWTTTTWWWWWWWTWAAAAAAWAAWTWWWTTWTTWTTTT 737

Qy   1060 aataattatagagctataacatgtttatttgacctcaataaaca 1103
Db    736 TTWWTTTWATTWAWTTTTTTTTTTTTTTTTTAAAAAAAAAAAA 693


RESULT 12
CNS0161D
LOCUS       CNS0161D                1225 bp    DNA     linear   GSS 26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
```

```
           BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
           fly), genomic survey sequence.
ACCESSION  AL106171
VERSION    AL106171.1  GI:5620504
KEYWORDS   GSS.
SOURCE     fruit fly.
  ORGANISM Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
           Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
           Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 1225)
  AUTHORS  Genoscope.
  TITLE    Direct Submission
  JOURNAL  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
           collaboration with the European Drosophila Genome Project (EDGP) -
           http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
           library (Dros BAC) was made by Alain Billaud at CEPH (Centre
           d'Etude du Polymorphisme Humain) with funding provided by a MRC
           project grant. The DNA was prepared from embryos by Alain Bucheton
           and Genevieve Payan. It has been constructed in the vector
           pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1. .1225
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN15C18"
                     /note="end : SP6"
BASE COUNT      266 a    128 c     38 g    368 t    425 others
ORIGIN
```

```
  Query Match             6.2%;  Score 69;  DB 12;  Length 1225;
  Best Local Similarity   31.6%;  Pred. No. 0.0029;
  Matches  135;  Conservative   93;  Mismatches  199;  Indels    0;  Gaps    0;

Qy     605 tagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatgggaagc 664
           :| |: :||:::|| :  : : || || |  |:|:  :| |  || |
Db     774 KAMAMNWAAHHWTTTYTWAAHAYNAAAAATTTAAAATCKCAAAMAMAAMAAAMMAAAAAC 833

Qy     665 caaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaaggaaaacc 724
           | : | || :  :: :::::::::  :| ::          |  || |||  |||
Db     834 CCMCCVCCKKKKDKKKKKKKKDDKDAAKRARADDRKAAAAAAAAATATAAAAAAAAAAAA 893

Qy     725 aatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttattgat 784
           ||   : ||:| ::   :| |: :  |  :|   :||  |:  | | | | : ::|  :
Db     894 AAAAWWWATTYTYYYAYAWAAAYAWATAAWWAWTTWTTAAAWWAAAAAAAAAAWAWWTTTY 953

Qy     785 aacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaatgattgt 844
           || |  : :|:  |     | || | |   : :     :: || ||| |:  |: || |
Db     954 AAAAAAWTWTWAAATAAWTTATTTTTTTTTAWWWTTTATWWATAATTTATWTTTWTTTTT 1013

Qy     845 ctttttccataaaaaagattactttccattcctttaggggaaaaaacccctaaatagctt 904
            ||:|   |:|||||| | ||  ||  :|:  ::|:       |     : | |    |
Db    1014 TTTWTAAAAWAAAAAAAAATATATTTTWTWAWWWTWTWATTTTTATATATWTAYTTTTAT 1073

Qy     905 catgtttccataatcagtactttatatttataaatgtatttattattattataagactgc 964
           | : :  :  ::   |: :|||:| ::: :::   ||||| |: ||  |:||: | :
Db    1074 ATTMWAWAWWATWWTTWTWTWTTWTTWWWTWWWTAATATTTTTWTTTTATWTAWAATWAT 1133

Qy     965 attttatttatatcattttattaatatggatttatttatagaaacatcattcgatattgc 1024
           ||   | :|:| | :: | || :||:|  || | |||||| |:| ::  ||  :|:::
Db    1134 ATAAAAAWTWTTTWWWATAATAWATWTATATATTTTTATAAAWAAWWTTTTWTWTWWWWT 1193

Qy    1025 tacttga 1031
           :  |: |
Db    1194 WTWTWWA 1200
```

```
RESULT  13
CNS000B8
LOCUS      CNS000B8              1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
           BACR01A24 of RPCI-98 library from Drosophila melanogaster (fruit
           fly), genomic survey sequence.
ACCESSION  AL063632
VERSION    AL063632.1  GI:4938680
KEYWORDS   GSS.
SOURCE     fruit fly.
  ORGANISM Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
           Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
           Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1  (bases 1 to 1101)
  AUTHORS  Genoscope.
  TITLE    Direct Submission
  JOURNAL  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
           BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
           - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
           collaboration with the Berkeley Drosophila Genome Project (BDGP).
           The BDGP is constructing a physical map of the Drosophila
           melanogaster genome using these BACs. For further information
           please see  http://www.fruitfly.org The BDGP Drosophila
           melanogaster BAC library was prepared by Kazutoyo Osoegawa and
           Aaron Mammoser in Pieter de Jong's laboratory in the Department of
           Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
           NY. The library is named RPCI-98 and was constructed by partial
           EcoRI digestion of Drosophila DNA provided by the BDGP from the
           isogenic strain y2; cn bw sp, the same strain used for the BDGP's
           P1 and EST libraries. A more detailed description of the library
           and how to order individual BAC clones, the entire library, or
           filters for hybridization from the BACPAC Resource Center can be
           found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR01A24"
                     /note="end : TET3"
BASE COUNT      228 a    114 c    110 g    512 t    137 others
ORIGIN
```

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  Query Match             6.1%;  Score 68.6;  DB 12;  Length 1101;
  Best Local Similarity   39.8%;  Pred. No. 0.0034;
  Matches  134;  Conservative   47;  Mismatches  156;  Indels    0;  Gaps    0;

Qy     755 tagactttctaagcatagatatttattgataacatttcattgtaactggtgttctataca 814
           |: | ::: : :  |:|  | ::| |   | : |||: ||| |      | |: | ||
Db     734 TWTATWWWTWTWTWAWAWTTTWWTTTATTTTRAATTWRATTTTKGTAATTTTWATTTADT 793

Qy     815 cagaaaacaatttatttttttaaataattgtctttttccataaaaaagattactttccatt 874
              :|   :||||:||:|: ||:::| | :|||| || |     ||   ||   ||
Db     794 TTTTTWATTTWTTATWTTWTWTATWWWTTTWWTTTTTWATTTATTTTTTTTWATTTTTTT 853

Qy     875 cctttaggggaaaaaacccctaaatagcttcatgtttccataatcagtactttatattta 934
           | :     |||||     |  |::  || | |||  ||  | : |: || |  | ||
Db     854 TTTAWTAAAAAAAAATTAAATTTAWWAWTTAAAWTTTTWATTTTTWATWWTTAAATTATA 913

Qy     935 taaatgtatttattattattataagactgcattttatttatatcattttattaatatgga 994
           |:  |   ::|  :| : |||     |   |||||||| | |  ||||:| :||:|  :
Db     914 TWTTTWATWWTTAWAAWTTTATTTWTTTTTTTTTTTATTTTTTTTTTTTTTWTAWATWTATW 973

Qy     995 tttatttatagaaacatcattcgatattgctacttgagtgtaaggctaatattgatattt 1054
           |||| :| ||  || :  |||  :|  :  |  ||  |  :|   | || ||  |  ||
Db     974 TTTAAWTTTATTAAAWATATTATWTTAWWATTTTTATATTAWAATTTTATTTTTTTTATT 1033

Qy    1055 atgacaataattatagagctataacatgtttatttga 1091
           |: : |:  : |:|  |     |    | ||| |:: |
Db    1034 AWTWWAWATWATWTTTATAATTTTTTTTTTTTTWWAA 1070
```

```
RESULT  14
CNS038CX
LOCUS       CNS038CX                639 bp    DNA     linear   GSS 15-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            005C19 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL232458
VERSION     AL232458.1  GI:7891593
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 639)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 639)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .639
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="005C19"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG005AB10XD1~end : T7"
BASE COUNT      210 a      3 c      5 g    381 t     40 others
ORIGIN

  Query Match             6.1%;  Score 68.2;  DB 12;  Length 639;
  Best Local Similarity   46.5%;  Pred. No. 0.004;
  Matches  148;  Conservative    6;  Mismatches  164;  Indels    0;  Gaps    0;

Qy     774 tatttattgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttt 833
           |||||||| ||    ||    | ||| |  |  |  | | |   |||| |  | | || |
Db      43 TATTTATTTATTTTTTTAACCTTTAATTATTTATAAAAAAAATAAAAATATATAAATTAT 102

Qy     834 taaataattgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccc 893
           ||||| ||| | |||||  | | ||||   || | |  :       |
Db     103 TAAATTATTTTWTTTTTAAAAATAAAATTATATTNTAAWANTNNNAANATNTTTNTTNNN 162

Qy     894 ctaaatagcttcatgtttccataatcagtactttatatttataaatgtatttattattat 953
               |     |:      |:|     |       | :|:| | | | | | || ||||
Db     163 NNTNNAANNNNAAWAAANTAAWANAANTTTTNNATAAAWTWTTANTATTTATTTTTTTAT 222

Qy     954 tataagactgcattttatttatatcatttttattaatatggatttatttatagaaacatca 1013
           | |    |  ||||| ||||| |  |||||||  | |   ||| |||||      |
Db     223 TTTTTTTTTTATTTTTTTTATTTTTTTTTATTTTTTTTTTTTTTTTTATTATTTTTTTT 282

Qy    1014 ttcgatattgctacttgagtgtaaggctaatattgatatttatgacaataattatagagc 1073
           ||  |||||  || || | |  ||   |  ||||  | ||| |    ||  || | |
Db     283 TTTTATATTTATATTTTATTAAAATTTTTTTATTTTTTTTTTTTATTTATTTTTTTTTATA 342

Qy    1074 tataacatgtttatttga 1091
           |:||  |  |  ||| |
Db     343 AAWAATTTTATATTTTTA 360


RESULT  15
CNS00FUH/c
LOCUS       CNS00FUH                996 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR31O21 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL071063
VERSION     AL071063.1  GI:4951105
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 996)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .996
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR31O21"
                     /note="end : TET3"
BASE COUNT      383 a    164 c     81 g    171 t    197 others
ORIGIN

  Query Match             6.1%;  Score 68.2;  DB 12;  Length 996;
  Best Local Similarity   36.7%;  Pred. No. 0.0041;
  Matches  109;  Conservative   61;  Mismatches  127;  Indels    0;  Gaps    0;

Qy     804 tgttctatacacagaaaacaatttatttttaaataattgtctttttccataaaaaagat 863
           | || |:   | | |||    ||:::|: ||::|| |:|: : : |: :  |:: ||   :
Db     990 TTTTTTWATAAAAAAAATWTTTTWWTWATTWMAAAAWTWAWAWATWAMATTWWTAATTTB 931

Qy     864 tactttccattcctttaggggaaaaaacccctaaatagcttcatgtttccataatcagta 923
           |  :  ::   ::    :::| ::|||     ||| |  :: || |||   :|||:    |
Db     930 TTTBGGSSGSSSSSGSGSSSGGRRAAAAAAAAAAAAAAAWWWWATTTTTTWTWAAWTTTAA 871

Qy     924 ctttatatttataaatgtatttattattattataagactgcattttatttatatcatttt 983
           ||::  ||:|: |::  ::|| || || || |        :|||: ||| | | ||||:
Db     870 RTTWRATTTWAWTAWWTAWWTTTTTTTTTTTTTTTTTTAATWDTTTWTTTTTTTTWATTTW 811

Qy     984 attaatatggatttatttatagaaacatcattcgatattgctacttgagtgtaaggctaa 1043
           ||:::|:   |::|  :| :: :| || |::  ||:||  |  ||   | |      |
Db     810 ATWWWTMAAWAWWTTAWTTWWTTWATATAAWYAAATWTTTTTTTTTTTTTTTTTKATWAAT 751

Qy    1044 tattgatatttatgacaataattatagagctataacatgtttatttgacctcaataa 1100
```

```
          ||:|    |||:|     | ::|||  :  | |    | ||| |||    | ::|:|
Db    750 TAWTTTATTTTWTATTTTTTWWTATTWWTTTTTTTATTWTTTTTTTTTTTTTWWTWA 694
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Search completed: September 23, 2002, 00:02:37
Job time: 1944 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 00:45:19 ; Search time 2215.22 Seconds
(without alignments)
10542.526 Million cell updates/sec

Title: US-09-746-375-1
Perfect score: 1116
Sequence: 1 tcgagttagaattgtctgca.....ataaacacttggatatccta 1116

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 14

Total number of hits satisfying chosen parameters: 151023

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1116	100.0	1116	6	AX151713	AX151713 Sequence
2	1116	100.0	1116	6	AX179578	AX179578 Sequence
3	1114	99.8	1152	6	AX092422	AX092422 Sequence
4	1114	99.8	1167	9	AF279437	AF279437 Homo sapi
5	1090	97.7	1132	6	AX048204	AX048204 Sequence
6	934	83.7	1139	6	AX054620	AX054620 Sequence
7	639	57.3	690	9	HSA277247	AJ277247 Homo sapi
8	636	57.0	8393	9	AF387519	AF387519 Homo sapi
c 9	636	57.0	133350	9	AC022511	AC022511 Homo sapi
c 10	636	57.0	191111	9	AC007458	AC007458 Homo sapi
11	250	22.4	135146	2	AC087562	AC087562 Pan trogl
12	207	18.5	5397	9	HSA277248	AJ277248 Homo sapi
c 13	66	5.9	135146	2	AC087562	AC087562 Pan trogl
14	35	3.1	778	6	AX179614	AX179614 Sequence
15	35	3.1	1119	6	AR165226	AR165226 Sequence
16	35	3.1	1121	10	MMU249491	AJ249491 Mus muscu
17	31	2.8	7445	6	AR165227	AR165227 Sequence
18	31	2.8	8270	10	MMU294727	AJ294727 Mus muscu
19	28	2.5	1111	6	AR16522B	AR16522B Sequence
20	28	2.5	1118	10	MMU249492	AJ249492 Mus muscu
21	28	2.5	5935	6	AR165234	AR165234 Sequence
22	28	2.5	5935	10	MMU294728	AJ294728 Mus muscu
23	27	2.4	36	6	AX151727	AX151727 Sequence
24	27	2.4	36	6	AX179593	AX179593 Sequence
c 25	24	2.2	24	6	AX179582	AX179582 Sequence
26	24	2.2	24	6	AX179583	AX179583 Sequence
c 27	24	2.2	33	6	AX151728	AX151728 Sequence
c 28	24	2.2	33	6	AX179594	AX179594 Sequence
29	24	2.2	5421	6	AX345034	AX345034 Sequence
c 30	23	2.1	23	6	AX179585	AX179585 Sequence
c 31	23	2.1	37	6	AX179598	AX179598 Sequence
c 32	23	2.1	50579	9	HS1086L22	AL109910 Human DNA
33	23	2.1	104607	8	ATT28J14	AL163652 Arabidops
c 34	23	2.1	160298	2	AL596442	AL596442 Homo sapi
35	22	2.0	39	6	AX179597	AX179597 Sequence
c 36	22	2.0	2640	6	AX211755	AX211755 Sequence
c 37	22	2.0	2640	6	AX212317	AX212317 Sequence
38	22	2.0	4702	3	SUT217G	M22207 T.gratilla
39	22	2.0	7304	6	AX281179	AX281179 Sequence
40	22	2.0	7304	6	AX356444	AX356444 Sequence
c 41	22	2.0	66606	2	AC101404	AC101404 Mus muscu
42	22	2.0	74342	8	AB020742	AB020742 Arabidops
43	22	2.0	78378	8	AC007260	AC007260 Arabidops
44	22	2.0	95364	5	AL591482	AL591482 Zebrafish
45	22	2.0	95769	8	AC013430	AC013430 Genomic s

ALIGNMENTS

RESULT 1
AX151713
LOCUS AX151713 1116 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 14 from Patent WO0140467.
ACCESSION AX151713
VERSION AX151713.1 GI:14533647
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1116)
AUTHORS Presnell,S.R., Xu,W., Kindsvogel,W. and Chen,Z.
TITLE Human cytokine receptor
JOURNAL Patent: WO 0140467-A 14 07-JUN-2001;
ZymoGenetics, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1116
/organism="Homo sapiens"
/db_xref="taxon:9606"
CDS 21. .560
/note="unnamed protein product"
/codon_start=1

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BASE COUNT      336 a    229 c    222 g    329 t
ORIGIN


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Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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RESULT   2
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LOCUS       AX179578                1116 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 1 from Patent WO0146422.
ACCESSION   AX179578
VERSION     AX179578.1  GI:15132010
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1116)
  AUTHORS   Presnell,S.R. and Kindsvogel,W.
  TITLE     Cytokine zcyto18
  JOURNAL   Patent: WO 0146422-A 1 28-JUN-2001;
            ZymoGenetics, Inc. (US)
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BASE COUNT      336 a    229 c    222 g    329 t
ORIGIN


  Query Match           100.0%;  Score 1116;  DB 6;  Length 1116;
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RESULT   3
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LOCUS       AX092422               1152 bp    DNA     linear   PAT 21-MAR-2001
DEFINITION  Sequence 153 from Patent WO0116318.
ACCESSION   AX092422
VERSION     AX092422.1  GI:13444525
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1152)
  AUTHORS   Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
            Wood,W.I.
  TITLE     Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
  JOURNAL   Patent: WO 0116318-A 153 08-MAR-2001;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN


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ACCESSION   AF279437
VERSION     AF279437.1  GI:10719561
KEYWORDS    .
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1167)
  AUTHORS   Xie,M.H., Aggarwal,S., Ho,W.H., Foster,J., Zhang,Z., Stinson,J.,
            Wood,W.I., Goddard,A.D. and Gurney,A.L.
  TITLE     Interleukin (IL)-22, a Novel Human Cytokine That Signals through
            the Interferon Receptor-related Proteins CRF2-4 and IL-22R
  JOURNAL   J. Biol. Chem. 275 (40), 31335-31339 (2000)
   PUBMED   10875937
REFERENCE   2  (bases 1 to 1167)
  AUTHORS   Xie,M.-H., Aggarwal,S., Ho,W.-H., Foster,J., Zhang,Z., Stinson,J.,
            Wood,W.I., Goddard,A.D. and Gurney,A.L.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2000) Molecular Biology, Genentech Inc., 1 DNA
            Way, South San Francisco, CA 94080, USA
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BASE COUNT      357 a    244 c    228 g    338 t
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Qy     61 ggaccctggccaccagctgcctccttctcttggccctcttggtacagggaggagcagctg 120
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Db     98 GGACCCTGGCCACCAGCTGCCTCCTTCTCTTGGCCCTCTTGGTACAGGGAGGAGCAGCTG 157

Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
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Db    158 CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCA 217

Qy    181 accgcaccttcatgctggctaaggaggctagcttggctgataacaacacagacgttcgtc 240
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Db    218 ACCGCACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAACAACACAGACGTTCGTC 277

Qy    241 tcattggggagaaactgttccacggagtcagtatgagtgagcgctgctatctgatgaagc 300
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Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Qy    421 ttgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtgaaaa 480
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Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Db    518 AGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTC 577

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
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Db    578 TGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTTCC 637

Qy    601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatggg 660
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Qy    661 aagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaagga 720
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Db    698 AAGCCAAACTCCATCATGATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGA 757

Qy    721 aaccaatgccactttgtttataagaccagaaggtagactttctaagcatagatatttat 780
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Db    758 AACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTCTAAGCATAGATATTTAT 817

Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Db    818 TGATAACATTTCATTGTAACTGGTGTTCTATACACAGAAAACAATTTATTTTTTTAAATAA 877

Qy    841 ttgtctttttccataaaaaagattactttccattcctttaggggaaaaaaccccctaaata 900
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Db    938 GCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTATTATTATTATAAGA 997

Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Db    998 CTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGATA 1057

Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Db   1058 TTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTATAGAGCTATAACA 1117

Qy   1081 tgtttatttgacctcaataaacacttggatatcc 1114
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Db   1118 TGTTTATTTGACCTCAATAAACACTTGGATATCC 1151


RESULT   5
AX048204
LOCUS       AX048204               1132 bp    DNA     linear   PAT 15-DEC-2000
DEFINITION  Sequence 44 from Patent WO0070049.
ACCESSION   AX048204
VERSION     AX048204.1  GI:11876994
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1132)
  AUTHORS   Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
            Azimzai,Y., Lu,D.A. and Patterson,C.
  TITLE     Extracellular signaling molecules
  JOURNAL   Patent: WO 0070049-A 44 23-NOV-2000;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1132
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ORIGIN


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Qy    901 gcttcatgtttccataatcagtactttatatttataaatgtatttattattattataaga 960
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Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Qy   1081 tgtttatttg 1090
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RESULT   6
AX054620
LOCUS       AX054620               1139 bp    DNA     linear   PAT 13-JAN-2001
DEFINITION  Sequence 1 from Patent WO0073457.
ACCESSION   AX054620
VERSION     AX054620.1  GI:12228184
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1139)
  AUTHORS   Parham,C.L., de waal Malefyt,R. and Marehalli,N.L.
  TITLE     Mammalian interleukin-10 homologs: il-d110 and il-d210
  JOURNAL   Patent: WO 0073457-A 1 07-DEC-2000;
            SCHERING CORPORATION (US)
FEATURES             Location/Qualifiers
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ORIGIN


  Query Match             83.7%;  Score 934;  DB 6;  Length 1139;
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Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattatagagctataaca 1080
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Qy   1081 tgtttat 1087
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RESULT   7
HSA277247
LOCUS       HSA277247               690 bp    mRNA    linear   PRI 21-DEC-2000
DEFINITION  Homo sapiens mRNA for interleukin 22 (IL-22 gene).
ACCESSION   AJ277247
VERSION     AJ277247.1  GI:9968293
KEYWORDS    IL-22 gene; interleukin 22.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 690)
  AUTHORS   Dumoutier,L., Van Roost,E., Colau,D. and Renauld,J.C.
  TITLE     Human interleukin-10-related T cell-derived inducible factor:
            molecular cloning and functional characterization as an
            hepatocyte-stimulating factor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (18), 10144-10149 (2000)
  MEDLINE   20420346
REFERENCE   2  (bases 1 to 690)
  AUTHORS   Renauld,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) Renauld J.C., UCL 74.59, Ludwig Institute
            for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
            BELGIUM
FEATURES             Location/Qualifiers
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ORIGIN


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Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcaccca 180
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Qy    301 aggtgctgaacttcacccttgaagaagtgctgttccctcaatctgataggttccagcctt 360
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Qy    361 atatgcaggaggtggtgcccttcctggccaggctcagcaacaggctaagcacatgtcata 420
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Qy    481 agcttggagagagtggagagatcaaagcaattggagaactggatttgctgtttatgtctc 540
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Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
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Db    592 TGAGAAATGCCTGCATTTGACCAGAGCAAAGCTGAAAAATGAATAACTAACCCCCTTTCC 651

Qy    601 ctgctagaaataacaattagatgccccaaagcgattttt 639
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RESULT   8
AF387519
LOCUS       AF387519               8393 bp    DNA     linear   PRI 14-JUN-2001
DEFINITION  Homo sapiens interleukin 22 (IL22) gene, complete cds.
ACCESSION   AF387519
VERSION     AF387519.1  GI:14423570
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 8393)
  AUTHORS   Rieder,M.J., Carrington,D.P., Chung,M.-W., Lee,K.L., Poel,C.L.,
            Yi,Q. and Nickerson,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-2001) Molecular Biotechnology, University of
            Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT     To cite this work please use:  SeattleSNPs. NHLBI Program for
            Genomic Applications, UW-FHCRC, Seattle, WA (URL:
            http://pga.mbt.washington.edu).
FEATURES             Location/Qualifiers
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                     6685. .6841)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   6683 AGCTTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTTGCTGTTTATGTCTC 6742

Qy    541 tgagaaatgcctgcatttgaccagagcaaagctgaaaaatgaataactaaccccctttcc 600
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Qy    661 aagccaaactccatcatgatgggtggattccaaatgaaccccctgcgttagttacaaagga 720
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Qy    721 aaccaatgccacttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
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Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Db   7163 CTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGAAACATCATTCGATA 7222

Qy   1021 ttgctacttgagtgtaaggctaatattgatatttatgacaataattattatagagctataaca 1080
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RESULT   9
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LOCUS       AC022511              133350 bp    DNA     linear   PRI 11-JUL-2001
DEFINITION  Homo sapiens 12 BAC RP11-71J4 (Roswell Park Cancer Institute Human
            BAC Library) complete sequence.
ACCESSION   AC022511
VERSION     AC022511.22  GI:14669924
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 133350)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R. and Gibbs,R.
TITLE Direct Submission
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 133350)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 133350)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Jul 11, 2001 this sequence version replaced gi:12656660.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT----------

--- Summary Statistics ---

Contig length:	150667
Phrap values in estimate:	149705
Average error rate (BCM-Phrap estimate):	1.52849e-05
Fraction of Phrap values less than 40 :	0.0163588
Number of consensus changing edits:	83
Number of N's in consensus :	0

--- Consensus changing edits ---

Position	Original+Context	Edited+Context
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7825	attatatatn(n)nngtatacta	attatatatg(t)gtgtatacta
7826	ttatatatnn(n)ngtatactat	ttatatatgt(g)tgtatactat
7827	tatatatnnn(n)gtatactata	tatatatgtg(t)gtatactata
7855	atatatatgc(n)acattttata	atatatatgc(a)acattttata
8162	agaccacttt(n)tgagatggca	agaccacttt(t)tgagatggca
10049	tgggcagatc(n)cnnnnngnnn	tgggcagatc(a)cctgaggtca
10051	ggcagatcnc(n)nnnngnnnnn	ggcagatcac(c)tgaggtcagg
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10112	ntactaaaaa(n)acaaaaatta	ctactaaaaa(t)acaaaaatta
10287	atggaagaga(n)tgtgggtata	atggaagaga(t)tgtgggtata
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19859	tgaatnaaaa(n)gcccaggtta	tgaattaaaa(t)gcccaggtta
19882	tttctatctc(n)ctgactnaan	tttctatctc(c)ctgactagat
19889	ctcnctgact(n)aannnnnnnt	ctccctgact(a)gatggccagt
19890	tcnctgactn(a)annnnnnntn	tccctgacta(g)atggccagtt
19892	nctgactnaa(n)nnnnnntnnn	cctgactaga(t)ggccagttcc
19893	ctgactnaan(n)nnnnntnnnn	ctgactagat(g)gccagttcca
19894	tgactnaann(n)nnnntnnnnc	tgactagatg(g)ccagttccat
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19902        nnnnnnntnn(n)ncnnnttnng    tggccagttc(c)attagggcag
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19963        ttccagnaaa(n)accacngttn    ttccagtaaa(t)accactgttt
19969        naaanaccac(n)gttnctctct    taaataccac(t)gtttctctct
19973        naccacngtt(n)ctctctctct    taccactgtt(t)ctctctctct
43356        actatcattg(n)agttatgagt    actatcattg(a)agttatgagt
61290        aagaccctgt(n)tcaaaaaaaa    aagaccctgt(c)tcaaaaaaaa
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93027        cagacatatg(a)gtgcatnctt    cagacatatg(t)gtgcatgctt
93034        atgagtgcat(n)cttgatntcc    atgtgtgcat(g)cttgatgtcc
93041        catncttgat(n)tccctattaa    catgcttgat(g)tccctcttaa
93047        tgatntccct(a)ttaaaactct    tgatgtccct(c)ttaaaactct
93107        attcatctca(n)tttcctctta    attcatctca(a)tttcctctta
105875       aaatgccatg(n)caatgtcagg    aaatgccatg(g)caatgtcagg
124584       aagtccatgt(n)ngtaggaact    aagtccatgt(a)cgtaggaact
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125786       ctggccaaca(n)ggtgaaaccc    ctggccaaca(t)ggtgaaaccc
125860       tcccagctac(n)nnnnaggctg    tcccagctac(t)cgggaggctg
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125863       cagctacnnn(n)naggctgagg    cagctactcg(g)gaggctgagg
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126773       ttttcttttg(c)ttttttcttt    ttttcttttg(t)ttttttcttt
126811       acggagtctc(n)ntctatnnnc    acggagtctc(g)ctctatcgcc
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126820       cnntctatnn(n)ccnggctgga    cgctctatcg(c)ccaggctgga
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Qy    721 aaccaatgccactttttgtttataagaccagaaggtagactttctaagcatagatatttat 780
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Qy    781 tgataacatttcattgtaactggtgttctatacacagaaaacaatttatttttttaaataa 840
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Qy    961 ctgcattttatttatatcattttattaatatggatttatttatagaaacatcattcgata 1020
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Qy   1081 tgtttatttgacctcaataaacacttggatatccta 1116
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Db   1633 TGTTTATTTGACCTCAATAAACACTTGGATATCCTA 1598


RESULT 10
AC007458/c
LOCUS       AC007458               191111 bp    DNA     linear   PRI 25-MAR-2000
DEFINITION  Homo sapiens 12q15 BAC RPCI11-444B24 (Roswell Park Cancer Institute
            Human BAC Library) complete sequence.
ACCESSION   AC007458
VERSION     AC007458.13  GI:5668755
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 191111)
  AUTHORS   Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y.,
            Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H.,
            Gorrell,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S.,
            Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W.,
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            Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L.,
            Rashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M.,
            Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W.,
            Zhou,X., Kucherlapati,R., Nelson,D., Nickerson,E. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 191111)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-MAY-1999) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 191111)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4  (bases 1 to 191111)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   5  (bases 1 to 191111)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-SEP-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   6  (bases 1 to 191111)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
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JOURNAL Submitted (25-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT On Jul 31, 1999 this sequence version replaced gi:5230396. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT----------

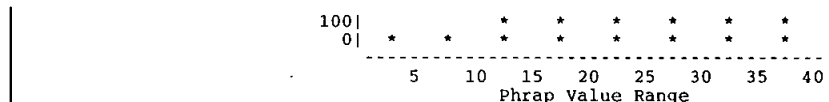
---------- Summary Statistics ----------

Contig length:	151624
Phrap values in estimate:	151315
Average error rate (BCM-Phrap estimate):	0.000165522
Fraction of Phrap values less than 40 :	0.020725
Number of consensus changing edits:	5
Number of N's in consensus :	0

---------- Consensus changing edits ----------

Position	Original+Context	Edited+Context
2273	ggccttcatt(n)tcaattgttt	ggccttcatt(t)tcaattgttt
5088	agatgggtgc(n)tactccttcc	agatgggtgc(c)tactccttcc
102880	ggtttcactg(n)gttaatcagg	ggtttcactg(t)gttaatcagg
123710	tcttataatt(n)tgtttatatg	tcttataatt(t)tgtttatatg
127972	ttttcttgag(n)gaatcctaag	ttttcttgag(t)gaatcctaag

--------- Distribution of Quality < 40 Bases ----------



Version: 1.01 qxfo.

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misc_feature	1. .82
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	/function="Overlaps with adjacent clone AC005294"
repeat_region	complement(3702. .4041)
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repeat_region	complement(4043. .7146)
	/rpt_family="L1PBb"
repeat_region	complement(7625. .7930)
	/rpt_family="L1PA15-16"
repeat_region	complement(8427. .8844)
	/rpt_family="L1M2"
repeat_region	complement(8860. .8988)
	/rpt_family="MLT1D"
repeat_region	complement(8997. .9284)
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repeat_region	complement(9927. .10097)
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repeat_region	10575. .10852
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Qy     601 ctgctagaaataacaattagatgccccaaagcgatttttttttaaccaaaaggaagatgggg 660
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Qy     661 aagccaaactccatcatgatgggtggattccaaatgaacccctgcgttagttacaaagga 720
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RESULT  11
AC087562
LOCUS       AC087562               135146 bp    DNA     linear   HTG 19-OCT-2001
DEFINITION  Pan troglodytes clone RP43-74I17, WORKING DRAFT SEQUENCE, 31
            unordered pieces.
ACCESSION   AC087562
VERSION     AC087562.4  GI:14190648
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 135146)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
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            Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
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            Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
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            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 135146)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 23, 2001 this sequence version replaced gi:12621390.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: ZUAE
                Center clone name: RP43-74I17
            -------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-primer Bodipy: 49% of reads
                Chemistry: Dye-terminator Big Dye: 51% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 134068 bases at least Q40
                Consensus quality: 143074 bases at least Q30
                Consensus quality: 148054 bases at least Q20
                Estimated insert size: 144346; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 31 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
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          * be preserved.
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          *    16597    22635: contig of 6039 bp in length
          *    22636    22735: gap of unknown length
          *    22736    28745: contig of 6010 bp in length
          *    28746    28845: gap of unknown length
          *    28846    34084: contig of 5239 bp in length
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          *    34185    39046: contig of 4862 bp in length
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          *    44981    45080: gap of unknown length
          *    45081    48686: contig of 3606 bp in length
          *    48687    48786: gap of unknown length
          *    48787    54719: contig of 5933 bp in length
          *    54720    54819: gap of unknown length
          *    54820    59584: contig of 4765 bp in length
          *    59585    59684: gap of unknown length
          *    59685    65244: contig of 5560 bp in length
          *    65245    65344: gap of unknown length
          *    65345    70092: contig of 4748 bp in length
          *    70093    70192: gap of unknown length
          *    70193    75303: contig of 5111 bp in length
          *    75304    75403: gap of unknown length
          *    75404    79784: contig of 4381 bp in length
          *    79785    79884: gap of unknown length
          *    79885    84754: contig of 4870 bp in length
          *    84755    84854: gap of unknown length
          *    84855    88649: contig of 3795 bp in length
          *    88650    88749: gap of unknown length
          *    88750    92541: contig of 3792 bp in length
          *    92542    92641: gap of unknown length
          *    92642    96461: contig of 3820 bp in length
          *    96462    96561: gap of unknown length
          *    96562   100892: contig of 4331 bp in length
          *   100893   100992: gap of unknown length
          *   100993   103932: contig of 2940 bp in length
          *   103933   104032: gap of unknown length
          *   104033   107186: contig of 3154 bp in length
          *   107187   107286: gap of unknown length
          *   107287   110219: contig of 2933 bp in length
          *   110220   110319: gap of unknown length
          *   110320   113001: contig of 2682 bp in length
          *   113002   113101: gap of unknown length
          *   113102   115998: contig of 2897 bp in length
          *   115999   116098: gap of unknown length
          *   116099   119333: contig of 3235 bp in length
          *   119334   119433: gap of unknown length
          *   119434   122281: contig of 2848 bp in length
          *   122282   122381: gap of unknown length
          *   122382   125109: contig of 2728 bp in length
          *   125110   125209: gap of unknown length
          *   125210   127912: contig of 2703 bp in length
          *   127913   128012: gap of unknown length
          *   128013   130629: contig of 2617 bp in length
          *   130630   130729: gap of unknown length
          *   130730   132831: contig of 2102 bp in length
          *   132832   132931: gap of unknown length
          *   132932   135146: contig of 2215 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-74I17"
BASE COUNT    40919 a  26449 c  25229 g  39519 t   3030 others
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  Query Match           22.4%;  Score 250;  DB 2;  Length 135146;
  Best Local Similarity 99.7%;  Pred. No. 1.6e-133;
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Qy     707 ttagttacaaaggaaaccaatgccacttttgtttataagaccagaaggtagacttttctaa 766
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Db   29041 TTAGTTACAAAGGAAACCAATGCCACTTTTGTTTATAAGACCAGAAGGTAGACTTTTTAA 29100

Qy     767 gcatagatatttattgataacatttcattgtaactggtgttctatacacagaaaacaatt 826
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Qy     827 tatttttaaataattgtctttttccataaaaaagattactttccattcctttaggggaa 886
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Db   29161 TATTTTTAAATAATTGTCTTTTTCCATAAAAAAGATTACTTTCCATTCCTTTAGGGGAA 29220

Qy     887 aaaacccctaaatagcttcatgtttccataatcagtactttatatttataaatgtattta 946
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Db   29221 AAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAATGTATTTA 29280

Qy     947 ttattattataagactgcattttatttatatcattttattaatatggatttatttataga 1006
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Db   29281 TTATTATTATAAGACTGCATTTTATTTATATCATTTTATTAATATGGATTTATTTATAGA 29340

Qy    1007 a 1007
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Db   29341 A 29341


RESULT  12
HSA277248
LOCUS       HSA277248               5397 bp    DNA     linear   PRI 30-MAY-2001
DEFINITION  Homo sapiens IL-22 gene for interleukin 22, exons 1a-5.
ACCESSION   AJ277248
VERSION     AJ277248.1  GI:11967707
KEYWORDS    IL-22 gene; interleukin 22.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5397)
  AUTHORS   Dumoutier,L., Van Roost,E., Ameye,G., Michaux,L. and Renauld,J.C.
  TITLE     IL-TIF/IL-22: genomic organization and mapping of the human and
            mouse genes
  JOURNAL   Genes and immunity. 1 (8), 488-494 (2000)
  MEDLINE   21069354
   PUBMED   11197690
REFERENCE   2  (bases 1 to 5397)
  AUTHORS   Renauld,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) Renauld J.C., UCL 74.59, Ludwig Institute
            for Cancer Research, Avenue Hippocrate, 74, B-1200 Brussels,
            BELGIUM
FEATURES             Location/Qualifiers
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                     /cell_type="EBV-transformed B cell"
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                VLFPQSDRFQPYMQEVVPFLARLSNRLSTCHIEGDDLHIQRNVQKLKDTVKKLGESGE
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     intron     858. .1288
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BASE COUNT     1525 a   1007 c   1187 g   1678 t
ORIGIN
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Query Match 18.5%; Score 207; DB 9; Length 5397;
Best Local Similarity 100.0%; Pred. No. 1.6e-108;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 ggaccctggccaccagctgcctccttctctttggccctcttggtacagggaggagcagctg 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 cgcccatcagctcccactgcaggcttgacaagtccaacttccagcagccctatatcacca 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    772 CGCCCATCAGCTCCCACTGCAGGCTTGACAAGTCCAACTTCCAGCAGCCCTATATCACCA 831

Qy    181 accgcaccttcatgctggctaaggagg 207
          |||||||||||||||||||||||||||
Db    832 ACCGCACCTTCATGCTGGCTAAGGAGG 858
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RESULT 13
AC087562/c
LOCUS       AC087562              135146 bp    DNA     linear   HTG 19-OCT-2001
DEFINITION  Pan troglodytes clone RP43-74I17, WORKING DRAFT SEQUENCE, 31
            unordered pieces.
ACCESSION   AC087562
VERSION     AC087562.4  GI:14190648
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      chimpanzee.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 135146)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
            Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
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            Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
            Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
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            Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
            Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
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            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 135146)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2001) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On May 23, 2001 this sequence version replaced gi:12621390.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: ZUAE
                Center clone name: RP43-74I17
            -------------- Summary Statistics
                Sequencing vector: M13; L08821
                Chemistry: Dye-primer Bodipy: 49% of reads
                Chemistry: Dye-terminator Big Dye: 51% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 134068 bases at least Q40
                Consensus quality: 143074 bases at least Q30
                Consensus quality: 148054 bases at least Q20
                Estimated insert size: 144346; sum-of-contigs estimation
                Quality coverage: 0x in Q20 bases; agarose-fp estimation
                Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 31 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *    10638    16496: contig of 5859 bp in length
            *    16497    16596: gap of unknown length
            *    16597    22635: contig of 6039 bp in length
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            *    22736    28745: contig of 6010 bp in length
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            *    28846    34084: contig of 5239 bp in length
            *    34085    34184: gap of unknown length
            *    34185    39046: contig of 4862 bp in length
            *    39047    39146: gap of unknown length
            *    39147    44980: contig of 5834 bp in length
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            *    45081    48686: contig of 3606 bp in length
            *    48687    48786: gap of unknown length
            *    48787    54719: contig of 5933 bp in length
            *    54720    54819: gap of unknown length
            *    54820    59584: contig of 4765 bp in length
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            *    59685    65244: contig of 5560 bp in length
            *    65245    65344: gap of unknown length
            *    65345    70092: contig of 4748 bp in length
            *    70093    70192: gap of unknown length
            *    70193    75303: contig of 5111 bp in length
            *    75304    75403: gap of unknown length
            *    75404    79784: contig of 4381 bp in length
            *    79785    79884: gap of unknown length
            *    79885    84754: contig of 4870 bp in length
            *    84755    84854: gap of unknown length
            *    84855    88649: contig of 3795 bp in length
            *    88650    88749: gap of unknown length
            *    88750    92541: contig of 3792 bp in length
            *    92542    92641: gap of unknown length
            *    92642    96461: contig of 3820 bp in length
            *    96462    96561: gap of unknown length
            *    96562   100892: contig of 4331 bp in length
            *   100893   100992: gap of unknown length
            *   100993   103932: contig of 2940 bp in length
            *   103933   104032: gap of unknown length
            *   104033   107186: contig of 3154 bp in length
            *   107187   107286: gap of unknown length
            *   107287   110219: contig of 2933 bp in length
            *   110220   110319: gap of unknown length
            *   110320   113001: contig of 2682 bp in length
            *   113002   113101: gap of unknown length
            *   113102   115998: contig of 2897 bp in length
            *   115999   116098: gap of unknown length
            *   116099   119333: contig of 3235 bp in length
            *   119334   119433: gap of unknown length
            *   119434   122281: contig of 2848 bp in length
            *   122282   122381: gap of unknown length
            *   122382   125109: contig of 2728 bp in length
            *   125110   125209: gap of unknown length
            *   125210   127912: contig of 2703 bp in length
            *   127913   128012: gap of unknown length
            *   128013   130629: contig of 2617 bp in length
            *   130630   130729: gap of unknown length
            *   130731   132831: contig of 2102 bp in length
            *   132832   132931: gap of unknown length
            *   132932   135146: contig of 2215 bp in length.
FEATURES             Location/Qualifiers
     source          1. .135146
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-74I17"
BASE COUNT    40919 a  26449 c  25229 g  39519 t   3030 others
ORIGIN


  Query Match             5.9%;  Score 66;  DB 2;  Length 135146;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-26;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    417 catattgaaggtgatgacctgcatatccagaggaatgtgcaaaagctgaaggacacagtg 476
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Db  47800 CATATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTG 47741

Qy    477 aaaaag 482
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Db  47740 AAAAAG 47735


RESULT  14
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LOCUS       AX179614                778 bp    DNA     linear   PAT 06-AUG-2001
DEFINITION  Sequence 37 from Patent WO0146422.
ACCESSION   AX179614
VERSION     AX179614.1  GI:15132040
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   Presnell,S.R. and Kindsvogel,W.
  TITLE     Cytokine zcyto18
  JOURNAL   Patent: WO 0146422-A 37 28-JUN-2001;
            ZymoGenetics, Inc. (US)
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ORIGIN


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RESULT  15
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LOCUS       AR165226                1119 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 7 from patent US 6274710.
ACCESSION   AR165226
VERSION     AR165226.1  GI:16238719
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
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REFERENCE   1  (bases 1 to 1119)
  AUTHORS   Dumoutier,L., Louhed,J. and Renauld,J.
  TITLE     Antibodies which specifically bind T Cell inducible factors (TIFs)
  JOURNAL   Patent: US 6274710-A 7 14-AUG-2001;
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Query Match 3.1%; Score 35; DB 6; Length 1119;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: September 23, 2002, 02:50:49
Job time: 7530 sec